

?d s1/3/1-12

Display 1/3/1

08504054 93214054

Mobilization of hematopoietic stem and progenitor cell subpopulations from the marrow to the blood of mice following cyclophosphamide and/or granulocyte colony-stimulating factor.

Neben S; Marcus K; Mauch P

Joint Center for Radiation Therapy, Harvard Medical School, Boston, MA 02115.

Blood (UNITED STATES) Apr 1 1993, 81 (7) p1960-7, ISSN 0006-4971

Journal Code: A8G

Languages: ENGLISH

Document type: JOURNAL ARTICLE

- end of record -

?

Display 1/3/2

08453069 93163069

Peripheral blood stem cell mobilization by cytokines.

Ahmed T; Wuest D; Ciavarella D

New York Medical College, Valhalla 10595.

J Clin Apheresis (UNITED STATES) 1992, 7 (3) p129-31, ISSN 0733-2459

Journal Code: HID

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL

- end of record -

?

Display 1/3/3

08392390 93102390

Peripheral blood stem cell mobilization after stem cell factor or G-CSF treatment: rapid enrichment for stem and progenitor cells using the CEPRATE immunoaffinity separation system.

Heimfeld S; Fogarty B; McGuire K; Williams S; Berenson RJ

CellPro, Incorporated, Bothell, Washington 98021.

Transplant Proc (UNITED STATES) Dec 1992, 24 (6) p2818, ISSN

0041-1345 Journal Code: WE9

Languages: ENGLISH

Document type: JOURNAL ARTICLE

- end of record -

?

Display 1/3/4

08095168 92233168

[The role of stem cell mobilization in the scope of autologous blood stem cell transplantation]

Die Rolle der Stammzell-Mobilisation im Rahmen der Autologen Blutstammzell-Transplantation (ABSZT).

Korbling M

M. D. Anderson Cancer Center, University of Texas, Houston.

Beitr Infusionther 1991, 28 p233-41, ISSN 1011-6974 Journal Code:

BZI

Languages: GERMAN Summary Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL English Abstract

- end of record -

?

Display 1/3/5

07865980 92003980

~~6/17~~

Medline
6/17-93

Transplantation with blood stem cells.
Zander AR; Lyding J; Bielack S
Department of Hematology-Oncology, Universitätskrankenhaus Eppendorf,
Hamburg, FRG.
Blood Cells 1991, 17 (2) p301-9, ISSN 0340-4684 Journal Code: A8H
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL

- end of record -

?

Display 1/3/6

07765556 91284556
Mobilization of haemopoietic stem cells by cyclophosphamide into the
peripheral blood of patients with haematological malignancies.
Shepherd KM; Charles P; Sage RE; Dale RM; Norman JE; Kotasek D; Gregg A;
Futter J
Department Haematology/Oncology, Queen Elizabeth Hospital, Woodville,
Australia.
Clin Lab Haematol 1991, 13 (1) p25-32, ISSN 0141-9854
Journal Code: DKF
Languages: ENGLISH
Document type: JOURNAL ARTICLE

- end of record -

?

Display 1/3/7

07408512 90315512
The median daily increment of leukocytes during hematopoietic recovery
reflects the myeloid progenitor cell yield during leukapheresis in
children.
Emminger W; Emminger-Schmidmeier W; Hocker P; Gerhartl C; Kundi M; Gadner
H
St. Anna Children's Hospital, Vienna, Austria.
Bone Marrow Transplant Jun 1990, 5 (6) p419-24, ISSN 0268-3369
Journal Code: BON
Languages: ENGLISH
Document type: JOURNAL ARTICLE

- end of record -

?

Display 1/3/8

07292259 90199259
Therapeutic efficacy of autologous blood stem cell transplantation
(AB SCT): the role of cytotoxic/cytokine stem cell mobilization.
Korbling M; Haas R; Knauf W; Holle R; Hunstein W
Institut f. Medizinische Biometrie, Heidelberg University, FRG.
Bone Marrow Transplant Jan 1990, 5 Suppl 1 p39-40, ISSN 0268-3369
Journal Code: BON
Languages: ENGLISH
Document type: CLINICAL TRIAL; JOURNAL ARTICLE

- end of record -

?

Display 1/3/9

06054168 87028168
Complement split product C5a mediates the lipopolysaccharide-induced
mobilization of CFU-s and haemopoietic progenitor cells, but not the
mobilization induced by proteolytic enzymes.
Molendijk WJ; van Oudenaren A; van Dijk H; Daha MR; Benner R
Cell Tissue Kinet Jul 1986, 19 (4) p407-17, ISSN 0008-8730
Journal Code: CQA
Languages: ENGLISH

- end of record -

?

Display 1/3/10

04259195 81087195

Pyran copolymer: effect of molecular weight on stem cell mobilization in mice.

Zander AR; Spitzer G; Verma DS; Ginzburg S; Dicke KA

Biomedicine May 1980, 33 (3) p69-72, ISSN 0300-0893 Journal Code: ASP

Contract/Grant No.: CA-24770; CA-23077

Languages: ENGLISH

Document type: JOURNAL ARTICLE

- end of record -

?

Display 1/3/11

03321676 77223676

Mobilization of B and T lymphocytes and haemopoietic stem cells by polymethacrylic acid and dextran sulphate.

van der Ham AC; Benner R; Vos O

Cell Tissue Kinet Jul 1977, 10 (4) p387-97, ISSN 0008-8730

Journal Code: CQA

Languages: ENGLISH

Document type: JOURNAL ARTICLE

- end of record -

?

Display 1/3/12

02860675 76041675

Polymethacrylic acid: induction of lymphocytosis and tissue distribution.

Ross WM; Martens AC; van Bekkum DW

Cell Tissue Kinet Sep 1975, 8 (5) p467-77, ISSN 0008-8730

Journal Code: CQA

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Set	Items	Description
S1	12	STEM(W)CELL(W)(MOBILIZ? OR PERIPHERALIZ?)
S2	22	VERY(W)LATE(W)ANTIGEN(W)4
S3	0	S2 AND STEM(W)CELL
S4	183	VASCULAR(W)CELL(W)ADHESION(W)MOLECULE
S5	1	S4 AND STEM(W)CELL

?

Display 5/3/1

08217769 92355769

Role of beta 1 and beta 2 integrins in the adhesion of human CD34hi stem cells to bone marrow stroma.

Teixido J; Hemler ME; Greenberger JS; Anklesaria P

Department of Tumor Virology, Dana Farber Cancer Institute, Boston, Massachusetts 02115.

J Clin Invest Aug 1992, 90 (2) p358-67, ISSN 0021-9738

Journal Code: HS7

Contract/Grant No.: CA-39851; DE-08798; CA42368

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Display 1/3/3 (Item 3 from file: 5)

BROSIS
+

9805466 BIOSIS Number: 44055466

PERIPHERAL BLOOD STEM CELL MOBILIZATION AFTER STEM CELL FACTOR OR G-CSF
TREATMENT RAPID ENRICHMENT FOR STEM AND PROGENITOR CELLS USING THE CEPRATE
IMMUNOAFFINITY SEPARATION SYSTEM

HEIMFELD S; FOGARTY R; MCGUIRE K; WILLIAMS S; BERENSON R J

CELLPRO INC., 22322 20TH AVE. SE, SUITE 100, BOTHELL, WASH. 98021.

FIRST INTERNATIONAL CONGRESS OF THE CELL TRANSPLANT SOCIETY, PITTSBURGH,
PENNSYLVANIA, USA, MAY 31-JUNE 3, 1992. TRANSPLANT PROC 24 (6). 1992.

2818. CODEN: TRPPA

Language: ENGLISH

Document Type: CONFERENCE PAPER

- end of record -

?

Display 1/3/5 (Item 5 from file: 5)

9769786 BIOSIS Number: 44019786

COMPARISON OF PERIPHERAL BLOOD STEM CELL MOBILIZATION BY THREE REGIMENS

JANSSEN W E; ELFENBEIN G J; LEE C; SMILEE R; CARTER R; PACH M; LEPARC G F
; SINALDI E; MASSARO P; ET AL

H. LEE MOFFITT CANCER CENT., UNIV. SOUTH FLA. COLL. MED., TAMPA, FLA.

45TH ANNUAL MEETING OF THE AMERICAN ASSOCIATION OF BLOOD BANKS, SAN
FRANCISCO, CALIFORNIA, USA, NOVEMBER 7-12, 1992. TRANSFUSION (ARLINGT) 32
(8 SUPPL.). 1992. 43S. CODEN: TRANA

Language: ENGLISH

Document Type: CONFERENCE PAPER

- end of record -

?

Display 1/3/6 (Item 6 from file: 5)

9347558 BIOSIS Number: 43092558

PERIPHERAL BLOOD STEM CELL MOBILIZATION AFTER STEM CELL FACTOR SCF ON
G-CSF TREATMENT RAPID ENRICHMENT FOR STEM AND PROGENITOR CELLS USING THE
CEPRATE IMMUNOAFFINITY SEPARATION SYSTEM

HEIMFELD S; ANDREWS R; ZSEBO K; FOGARTY B; MCGUIRE K; WILLIAMS S;
BERENSON R

CELLPRO INC., BOTHELL, WASH.

XXI ANNUAL MEETING OF THE INTERNATIONAL SOCIETY FOR EXPERIMENTAL
HEMATOLOGY, PROVIDENCE, RHODE ISLAND, USA, JULY 26-30, 1992. EXP HEMATOL (N
Y) 20 (6). 1992. 748. CODEN: EXHMA

Language: ENGLISH

Document Type: CONFERENCE PAPER

- end of record -

?

Display 1/3/7 (Item 7 from file: 5)

8884735 BIOSIS Number: 42109735

PERIPHERAL BLOOD STEM CELL MOBILIZATION RAPID ENRICHMENT OF PROGENITOR
CELLS USING A UNIQUE BIOTIN-AVIDIN IMMUNOAFFINITY SEPARATION SYSTEM

HEIMFELD S; RENSINGER W; FOGARTY B; MCGUIRE K; WILLIAMS S; ZSEBO K;
BERENSON R

CELLPRO INC., BOTHELL, WASH. 98021.

KEYSTONE SYMPOSIUM ON HEMATOPOIESIS, TAMARRON, COLORADO, USA, FEBRUARY
27-MARCH 5, 1992. J CELL BIOCHEM SUPPL 0 (16 PART C). 1992. 65. CODEN:
JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

- end of record -

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Display 1/3/8 (Item 8 from file: 5)

8871887 BIOSIS Number: 42096887

PERIPHERAL BLOOD STEM CELL MOBILIZATION RAPID ENRICHMENT OF PROGENITOR

CELLS USING A UNIQUE BIOTIN AVIDIN IMMUNOAFFINITY SEPARATION SYSTEM
 BERENSON R; ANDREWS R; BENSINGER W; FOGARTY B; MCGUIRE K; WILLIAMS S;
 HEIMFELD S
 CELLPRO INC., BOTHELL, WASHINGTON 98021, USA.
 KEYSTONE SYMPOSIUM ON BONE MARROW TRANSPLANTATION, KEYSTONE, COLORADO,
 USA, JANUARY 19-26, 1992. J CELL BIOCHEM SUPPL 8 (16 PART A). 1992. 189.
 CODEN: JCBSD
 Language: ENGLISH
 Document Type: CONFERENCE PAPER

- end of record -

?
 Display 1/3/12 (Item 12 from file: 5)

7329393 BIOSIS Number: 38109914
 THERAPEUTIC EFFICACY OF AUTOLOGOUS BLOOD STEM CELL TRANSPLANTATION ABSC
 THE ROLE OF CYTOTOXIC-CYTOKINE STEM CELL MOBILIZATION
 KOERBLING M; HAAS R; KNAUF W; HOLLE R; HUNSTEIN W
 MED. KLINIK POLIKLINIK V, INST. F. MED. BIOMETRIC, HEIDELBERG UNIV., FRG.
 INTERNATIONAL SYMPOSIUM ON PERIPHERAL BLOOD STEM CELL AUTOGRAFTS,
 MULHOUSE, FRANCE, OCTOBER 15-17, 1989. BONE MARROW TRANSPLANT 5 (SUPPL. 1).
 1990. 39-40. CODEN: BMTRE
 Language: ENGLISH
 Document Type: CONFERENCE PAPER

- end of record -

?
 Display 1/3/13 (Item 13 from file: 5)

7329385 BIOSIS Number: 38109906
 APPROACHES TO BLOOD STEM CELL MOBILIZATION INITIAL AUSTRALIAN CLINICAL
 RESULTS
 JUTTNER C A; TO L B; HAYLOCK D N; DYSON P G; BRADSTOCK K F; DALE B M;
 ENNO A; SAGE R E; SZER J; TOOGOOD I R G
 LEUKAEMIA RES. UNIT, IMVS, FROME RD., ADELAIDE, SOUTH AUSTRALIA, AUST.
 5000.
 INTERNATIONAL SYMPOSIUM ON PERIPHERAL BLOOD STEM CELL AUTOGRAFTS,
 MULHOUSE, FRANCE, OCTOBER 15-17, 1989. BONE MARROW TRANSPLANT 5 (SUPPL. 1).
 1990. 22-24. CODEN: BMTRE
 Language: ENGLISH
 Document Type: CONFERENCE PAPER

- end of record -

?
 Display 1/3/16 (Item 16 from file: 5)

2965749 BIOSIS Number: 69003156
 THE MECHANISM OF HEMOPOIETIC STEM CELL MOBILIZATION A ROLE OF THE
 COMPLEMENT SYSTEM
 WILSCHUT I J C; ERKENS-VERSLUIS M E; PLOEMACHER R E; BENNER R; VOS O
 DEP. CELL BIOL. GENET., ERASMUS UNIV., P.O. BOX 1738, ROTTERDAM, NETH.
 CELL TISSUE KINET 12 (3). 1979. 299-312. CODEN: CTKIA
 Full Journal Title: Cell and Tissue Kinetics
 Language: ENGLISH

- end of display -

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Set	Items	Description
S1	19	STEM(W)CELL(W)(MOBILIZ? OR PERIPHERALIZ?)
S2	38	VERY(W)LATE(W)ANTIGEN(W)4
S3	0	S2 AND STEM(W)CELL
S4	252	VASCULAR(W)CELL(W)ADHESION(W)MOLECULE
S5	0	S4 AND STEM(W)CELL
S6	0	S1 AND S2
S7	0	S1 AND S4

7754915 BIOSIS Number: 90122915

VASCULAR CELL ADHESION MOLECULE-1 MEDIATES LYMPHOCYTE ADHERENCE TO
CYTOKINE-ACTIVATED CULTURED HUMAN ENDOTHELIAL CELLS

CARLOS T M; SCHWARTZ B R; KOVACH N L; YEE E; ROSSO M; OSBORN L; CHI-ROSSO
G; NEWMAN B; LOBB R; HARLAN J M

DIV. HEMATOL., ZA-34, HARBORVIEW MED. CENT., 325 9TH AVE., SEATTLE, WASH.
98104.

BLOOD 76 (5). 1990. 965-970. CODEN: BLOOA

Full Journal Title: Blood

Language: ENGLISH

L6

5 L1 AND L4 AND L5

APS

=> d 1-5

1. 5,188,959, Feb. 23, 1993, Extracellular matrix protein adherent T cells; Allan B. Haberman, 435/240.243, 4, 240.2 [IMAGE AVAILABLE]
2. 5,187,193, Feb. 16, 1993, Method for stimulating transplanted bone marrow cells; Richard F. Borch, et al., 514/476 [IMAGE AVAILABLE]
3. 5,169,765, Dec. 8, 1992, Method for stimulating production of bone marrow cell growth factors using dithiocarbamates; Richard F. Borch, et al., 435/70.4, 69.5, 69.52 [IMAGE AVAILABLE]
4. 4,965,195, Oct. 23, 1990, Interleukin-7; Anthony E. Namen, et al., 435/69.52, 91, 172.1, 172.3, 320.1; 530/350, 351; 536/24.3, 24.31 [IMAGE AVAILABLE]
5. 4,808,402, Feb. 28, 1989, Method and compositions for modulating neovascularization; Samuel J. Leibovich, et al., 424/78.06, 423, 618; 514/2 [IMAGE AVAILABLE]

=>

(FILE 'USPAT' ENTERED AT 11:27:00 ON 17 JUN 93)

L1 58124 S BLOOD
L2 0 S STEM(W)CELL#(W)(MOBILIZ? OR PERIPHERALIZ?)
L3 0 S STEM(W)CELL#(W)(MOBILIZ?)
L4 145 S STEM(W)CELL
L5 154 S CYTOKINE
L6 5 S L1 AND L4 AND L5

=>

d 18 1-3

1. 5,188,959, Feb. 23, 1993, Extracellular matrix protein adherent T cells; Allan B. Haberman, 435/240.243, 4, 240.2 [IMAGE AVAILABLE]
2. 4,965,195, Oct. 23, 1990, Interleukin-7; Anthony E. Namen, et al., 435/69.52, 91, 172.1, 172.3, 320.1; 530/350, 351; 536/24.3, 24.31 [IMAGE AVAILABLE]
3. 4,808,402, Feb. 28, 1989, Method and compositions for modulating neovascularization; Samuel J. Leibovich, et al., 424/78.06, 423, 618; 514/2 [IMAGE AVAILABLE]

=>

Teng, S
977702
Seqs. 1 & 2

Seq. 1

> 0 <
0| 0 IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-07-977-702-1-ngs.res made by shears on Tue 15 Jun 93 11:23:42-PDT.

Query sequence being compared:US-07-977-702-1 (1-360)
Number of sequences searched: 25646
Number of scores above cutoff: 4455

Results of the initial comparison of US-07-977-702-1 (1-360) with:
Data bank : N-GeneSeq 10, all entries

10000-#
-
N -
U 5000- #
M -
B -
E - **
R - **
- *
D -
F 1000- *
-
S *
E 500- *
Q - *
U -
E -
N - *
C - *
E -
S 100-
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10- *
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- *
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5- *
- ***
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		**** 21 standard deviations above mean ****				
1. 011098	Encodes gamma heavy chain of	861	309	316	21.40	0
	**** 18 standard deviations above mean ****					
2. 010381	Chimeric MAb 9.2.27 heavy cha	363	270	279	18.54	0
	**** 17 standard deviations above mean ****					
3. 008607	Co-1 Heavy Chain V Region (mo	471	259	265	17.73	0
4. 022736	RSV19 VH.	348	256	299	17.51	0
5. 028739	cDNA of VH425 antibody cloned	501	256	269	17.51	0
	**** 16 standard deviations above mean ****					
6. 023863	ScFvB18 construct mutant #6.	770	236	280	16.05	0
7. 023862	ScFvB18 construct mutant #5.	770	236	280	16.05	0
8. 023861	ScFvB18 construct mutant #4.	770	236	280	16.05	0
9. 023860	ScFvB18 construct mutant #3.	770	236	280	16.05	0
10. 023859	ScFvB18 construct mutant #2.	770	236	280	16.05	0

11. Q21100	ScFvB18 construct.	770	236	280	16.05	0
**** 15 standard deviations above mean ****						
12. Q23858	ScFvB18 construct mutant #1.	770	234	279	15.90	0
13. Q15164	VH186 region of anti-nitrophe	458	233	277	15.83	0
14. Q06227	VH domain of antibody C again	345	229	245	15.53	0
15. N91482	Genomic to cDNA junction (V47	349	228	269	15.46	0
16. Q12013	Sequence encoding mouse MAb 2	477	226	259	15.31	0
17. Q12057	Sequence encoding heavy chain	477	226	259	15.31	0
18. Q27141	ICAM-1 inhibiting peptide 2.	387	225	263	15.24	0
19. Q06957	Genomic sequence encoding hea	2675	225	260	15.24	0
20. N91820	DNA sequence of the V and J r	443	224	262	15.17	0
21. Q28263	Fv(FRP51)-ETA fusion gene.	2012	223	270	15.09	0
22. Q28260	FWP51 fusion gene.	748	222	269	15.02	0
23. Q12637	Monoclonal antibody OK3T heav	1570	222	268	15.02	0
**** 14 standard deviations above mean ****						
24. Q28258	FWP51 heavy chain variable do	342	218	259	14.73	0
25. N91146	2H7 VH sequence.	458	218	266	14.73	0
26. N70968	Sequence of the anti-hepatiti	420	217	264	14.65	0
27. N70967	Sequence of the anti-hepatiti	420	217	264	14.65	0
28. Q04261	Encodes Colon Cancer monoclon	456	217	239	14.65	0
29. N70971	2H7 VH sequence which contain	459	217	265	14.65	0
30. Q23342	Murine heavy chain variable r	354	216	261	14.58	0
31. N91645	Heavy chain of monoclonal ant	540	216	270	14.58	0
32. Q04040	Anti-Leu 3a heavy chain varia	765	216	262	14.58	0
33. Q04262	Encodes Colon Cancer monoclon	416	215	239	14.51	0
34. Q08609	ME4 Heavy Chain V Region (mou	492	215	261	14.51	0
35. Q04463	Heavy chain variable region o	361	214	238	14.43	0
36. Q04258	Sequence homologous to TAG72	982	214	252	14.43	0
37. Q28522	Hypercalcaemia agent cDNA por	356	213	251	14.36	0
38. Q24790	Anti-Tac antibody heavy chain	433	213	247	14.36	0
39. Q05600	Anti-Tac heavy chain variable	433	213	247	14.36	0
40. Q05554	Sequence encoding variable re	446	213	233	14.36	0

1. US-07-977-702-1 (1-360)

Q11098 Encodes gamma heavy chain of T84.66 monoclonal ant

ID Q11098 standard; DNA; 861 BP.
AC Q11098;
DT 08-MAY-1991 (first entry)
DE Encodes gamma heavy chain of T84.66 monoclonal antibody.
KW MAb T84.66; gamma heavy chain; carcinoembryonic antigen; CEA;
KW human adenocarcinoma; mouse-human chimaeric antibody; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT exon 272..317
FT /*tag= a
FT intron 318..395
FT /*tag= b
FT exon 396..770
FT /*tag= c
FT promoter 109..118
FT /*tag= d
FT /note= "putative"
FT promoter 121..127
FT /*tag= e
FT /note= "putative"
FT promoter 160..166
FT /*tag= f
FT /note= "putative"
FT promoter 169..176
FT /*tag= g
FT /note= "putative"
PN W09101990-A.
PD 21-FEB-1991.
PF 19-JUL-1990; U04049.

PA (CITY) CITY OF HOPE.
 PI Shively JE, Riggs AD, Neumaier M;
 DR WPI: 91-073486/10.
 DR P-PSDB; R11384.
 PT Novel anti-CEA antibody - comparable to ATCC Accession No. BH
 PT 8747, produced by recombinant DNA, used in diagnosis of tumours
 PS Claim 4; Page 18; 24pp; English.
 CC The heavy chain variable region of murine MAb 84.66 was cloned and
 CC sequenced as follows: Hybridoma DNA was extracted, completely
 CC restricted with EcoRI and run on a gel. Fragments were extracted and
 CC ligated in the EcoRI site of Lambda-ZAP. Phage were packaged and plated.
 CC Plaque screening was with a 991bp XbaI fragment from the mouse
 CC enhancer region, a 1.5kb cDNA fragment from the heavy chain
 CC constant region gene of hybridoma CEA.66-E3 and a 5.4kb EcoRI
 CC fragment containing an aberrantly rearranged heavy chain from
 CC Sp2/0. Positive clones were further characterised by hybridisation
 CC to J-region oligonucleotides (see Q10842-Q10846) and sequenced. The
 CC murine gamma variable region gene was used to produce mouse V-human C
 CC antibodies with high affinity for CEA. Chimaeric murine-human anti-
 CC CEA Abs are used to diagnose human colon adenocarcinomas.
 CC See also Q10834-Q10841 and Q10847-8.
 SQ Sequence 861 BP; 213 A; 208 C; 203 G; 237 T;

Initial Score = 309 Optimized Score = 316 Significance = 21.40
 Residue Identity = 88% Matches = 322 Mismatches = 33
 Gaps = 10 Conservative Substitutions = 0

```

                                X      10      20
                                GTCAAACTGCAGCAGTCTGGGG
                                || | ||||| ||||| |||||
  GTGACAGTGGCAATCACTTTGCCTTTCTTTCTACAGGGGTCAATTGAGGTTGAGCTGCAGCAGTCTGGGG
360      370      380      390      400      410      420      430

      30      40      50      60      70      80      90
  CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  CAGAGCTTGTGGAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
      440      450      460      470      480      490      500

      100      110      120      130      140      150      160
  ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAATGGATTGGAAGGATTGATCCTGCGAATGGTA
      510      520      530      540      550      560      570

      170      180      190      200      210      220      230
  ATACTAAATATGACCCGAAGTTCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  ATAGTAAATATGTCCCGAAGTTCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
      580      590      600      610      620      630      640

      240      250      260      270      280      290      300
  TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGGAATGTGGGTATCAACG-
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  TGCAGCTCACCAGCCTGACATCTGAGGACACTGCCGTCTATTATTGTGC-TCCG---TTTGGTTA-CTACGT
      650      660      670      680      690      700      710

      310      320      330      340      350      X
  ----GGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
  | ||||| ||| || ||||| ||||| ||| | ||||| ||||| |||||
  GTCTGACTATGCTATGGCCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGGTAAGAATGGCCTCTC
      720      730      740      750      760      770      780

  CAGGTCTTTATTTTAAACCTTTGTATGGACTTT
      790      800      810
  
```

2. US-07-977-702-1 (1-360)

Q10381 Chimeric MAb 9.2.27 heavy chain variable region DN

ID Q10381 standard; DNA; 363 BP.
AC Q10381;
DT 15-APR-1991 (first entry)
DE Chimeric MAb 9.2.27 heavy chain variable region DNA sequence.
KW Chimeric antibodies; human glycoprotein antigen; melanoma; cancer;
KW ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 1..363
FT /*tag= a
FT /product= H-chain V-region of MAb 9.2.27
PN EP-411893-A.
PD 06-FEB-1991.
PF 31-JUL-1990; 308402.
PR 31-JUL-1989; US-387665.
PA (ELIL) ELI LILLY & CO.
PI Beavers LS, Bumol TF, Gadski RA;
DR WPI: 91-038771/06.
DR P-PSDB; R10541.
PT Monoclonal antibody contg. recombinant DNA - binds to human
PT chondroitin sulphate proteoglycan on melanoma cells for melanoma
PT treatment and diagnosis
PS Claim 11; page 18; 33pp; English.
CC This sequence, contained in vector pG4G21, is ligated to a DNA
CC sequence encoding a human heavy (H) chain constant (C) region, in
CC the construction of pN9.2.27G1. This vector is used to transform
CC host cells, in conjunction with vector pG9.2.27K contg. murine
CC light (L) chain variable (V) region and human L- chain C- region.
CC The resulting host cell expresses the chimeric antibody 9.2.27
CC which is directed against proteoglycans of human melanoma cells.
CC This chimeric monoclonal antibody (MAb) is useful in the diagnosis
CC and treatment of melanoma. The use of human C-regions avoids the
CC problems associated with murine monoclonals e.g. rapid clearance
CC from the bloodstream due to anti-self recognition.
CC See also Q10379-81 and Q10382-84.
SQ Sequence 363 BP; 88 A; 87 C; 105 G; 83 T;

Initial Score = 270 Optimized Score = 279 Significance = 18.54
Residue Identity = 78% Matches = 285 Mismatches = 72
Gaps = 6 Conservative Substitutions = 0

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X      10      20      30      40      50      60
GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGCCTCAAGTTGTCTGCACAGCT
||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
CAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCCTCAAGATTTCCTGCAAAGCT
X      10      20      30      40      50      60      70

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70      80      90     100     110     120     130     140
TCTGGCTTCAACATTAAAGA-CACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGAT
||||| | |||| | | | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TCTGGCTAC-GCATTCACTAGGTCTTGGATGAACCTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGACTGGAT
      80      90     100     110     120     130     140

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      150     160     170     180     190     200     210
TGGAAGGATTGATCCTGCGAG-TGGCGATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAG
|||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
TGGACGGATTATCCTG-GAGATGGAGATACTAACTACAATGGGAAGTTCAAGGGCAAGGCCACTGACTG
      150     160     170     180     190     200     210

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      220     230     240     250     260     270     280
CGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACT

```

CAGACAAATCCTCCAGCACAGCCTACATGCAGGTGAGCAGCCTGACCTCTGTGGACTCTGCGGTCTATTCT
 220 230 240 250 260 270 280

```

      360
TCCTCA
|||||
TCCTCA
360  X

```

```

70      80      90      100     110 X    120     130
30      40      50      60      70      80      90
CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAA--AGACAC
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCTTCTGGATAC-ACATTACTAGCTAT
140      150      160      170      180      190      200

100      110      120      130      140      150      160
CTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
GT-TATGCACTGGGTGAAGCAGAAGCCTGGGCAGGGCCTTGAGTGGATTGGATATATTATCCTTACAATGA
210      220      230      240      250      260      270

170      180      190      200      210      220      230
CGATACTAAATATGACCCGAAGTTCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
TGGTACTAGTTACAATGAGCCCTTCAAAGGCAAGGCCCACTGACTTCAGACAAATCCTCCAGCACAGCCTA
280      290      300      310      320      330      340

240      250      260      270      280      290      300
GCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGC-AGACGGA---ATGTGGGTAT
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CATGGAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTACTGTGCAAGGAGGATCTACTTTGATTA
350      360      370      380      390      400      410

310      320      330      340      350      X
CAACGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CTCC----TATGTTATGGACTACTGGGGTCAAGGAACCTCGGTACCGTCTCCTCA
420      430      440      450      460      470

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4. US-07-977-702-1 (1-360)

Q22736 RSV19 VH.

ID Q22736 standard; DNA; 348 BP.
AC Q22736;
DT 13-AUG-1992 (first entry)
DE RSV19 VH.
KW VH; VK; donor; antibody; CDR; epitope; NEW; REI;
KW fusion protein; F protein; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT misc_feature 91..105
FT /*tag= a
FT /label= CDR1
FT misc_feature 149..199
FT /*tag= b
FT /label= CDR2
FT misc_feature 296..316
FT /*tag= c
FT /label= CDR3
FT primer_bind 2..23
FT /*tag= d
FT /note= "corresponds to primer sequence used"
FT primer_bind 316..349
FT /*tag= e
FT /note= "corresponds to primer sequence used"
PN W09204381-A.
PD 19-MAR-1992.
PF 11-SEP-1991; G01554.
PR 11-SEP-1990; GB-019812.
PA (SCOT-) SCOTGEN LTD.
PI Harris WJ, Tempest PR, Taylor G;
DR WPI; 92-114306/14.

DR P-F508: R24807.
 PT New altered antibodies with donor MAb binding specificity for RSV
 PT - for treatment and prevention of human respiratory syncytial
 PT virus infection
 PS Disclosure; Fig 1; 72pp; English.
 CC The sequences of RSV19 VH and VK are represented in 022736 and 022737
 CC respectively. The donor antibody RSV19 is directed against epitope
 CC 417-438 of the fusion protein (F). The CDRs were identified (see
 CC features), then the murine CDRs transferred to human frameworks by
 CC site-directed mutagenesis, using as DNA templates human framework
 CC regions of the NEW (heavy) and REI (light) proteins.
 CC The altered antibodies are used to prevent or treat RSV infections
 CC in humans, e.g. for prevention they are given (each 6 weeks during
 CC the RSV season) at 1-20 mg/kg parenterally or 0.2-2 mg/kg
 CC intranasally. Since the antibodies are predominantly
 CC human, they are unlikely to cause much immune response.
 SQ Sequence 348 BP; 84 A; 91 C; 95 G; 76 T;
 SQ 2 Others;

Initial Score = 256 Optimized Score = 299 Significance = 17.51
 Residue Identity = 84% Matches = 305 Mismatches = 40
 Gaps = 15 Conservative Substitutions = 0

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      X      10      20      30      40      50      60
      GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCT
      ||| | ||||| ||||| ||||| ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
CAGGTCCAGCTGCAGSAGTCWGGGACAGAGCTTGAGAGGTGAGGGGCCTCAGTCAAGTTGTCCTGCACAGCT
      X      10      20      30      40      50      60      70

70      80      90      100     110     120     130     140
TCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TCTGGCTTCAACATTAAAGACTACTATATGCACTGGATGAAGCAGAGGCCTGACCAGGGCCTGGAGTGGATT
      80      90      100     110     120     130     140

      150     160     170     180     190     200     210
GGAAGGATTGATCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCG
||| ||||| ||||| ||| ||| ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
GGATGGATTGATCTGAGAATGATGATGTTCAATATGCCCGAAGTTCCAGGGCAAGGCCACTATGACTGCA
      150     160     170     180     190     200     210

      220     230     240     250     260     270     280
GACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GACACGTCCTCCAACACAGCCTACCTGCAGCTCACCAGCCTGACATTTGAGGACACTGCCGTCTATTTCTGT
      220     230     240     250     260     270     280

      290     300     310     320     330     340     350
GCAGACGGAATGTGGGTATCAACGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCC
      |||      ||| ||| ||| | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
-----AAT-----TCATGGGGAGTGACTTTGACCACTGGGGCCAAGGGACCACGGTCACCGTCTCC
      290      300      310      320      330      340

360
TCA
|||
TCA
X
  
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5. US-07-977-702-1 (1-360)
 028739 cDNA of VH425 antibody cloned into pUC18.

ID 028739 standard; DNA; 501 BP.
 AC 028739;
 DT 01-MAR-1993 (first entry)

DE cDNA of VH425 antibody cloned into pUC18.
 KW Monoclonal antibody; complementarity determining region; framework;
 KW antigens; tumour; melanoma; carcinoma; glioma; variable; heavy;
 KW light; chain; ss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 30..450
 FT /*tag= a
 FT sig_peptide 30..87
 FT /*tag= b
 FT mat_peptide 88..450
 FT /*tag= c
 FT primer_bind 10..32
 FT /*tag= d
 FT /note= "3'-5' PCR primer binding site"
 FT primer_bind 12..32
 FT /*tag= e
 FT /note= "PCR primer binding site"
 FT primer_bind 436..465
 FT /*tag= f
 FT /note= "3'-5' PCR primer binding site"
 PN W09215683-A.
 PD 17-SEP-1992.
 PF 04-MAR-1992; E00480.
 PR 06-MAR-1991; EP-103389.
 PA (MERE) MERCK PATENT GMBH.
 PI Bendig MM, Kettleborough CA, Saldanha J;
 DR WPI; 92-331729/40.
 DR P-PSBD; R27049.
 PT Human monoclonal antibodies binding to human receptors - for
 PT treatment and diagnosis of tumours, e.g. melanoma and carcinoma
 PS Disclosure; Fig 2; 89pp; English.
 CC The cDNA sequence encoding the variable heavy chain of monoclonal
 CC antibody 425 was prepd. synthetically and mutations made to the 5'
 CC and 3' ends to allow for cloning into HCMV expression vectors.
 CC Donor splice sites were recreated in the 3' flanking regions to
 CC allow correct splicing of the variable and constant regions. The
 CC 5' sequence was altered to introduce an initiation codon. These
 CC mutations were carried out using the PCR primers shown in the
 CC features table. The cloned chimeric antibody contg. 425 VL and
 CC 425 VH regions were cotransfected into COS cells to confirm cloning
 CC of the correct mouse base variable sequence. The cloned antibody
 CC may be used int the prodn.of reshaped or humanised antibodies which
 CC are less immunogenic than native antibodies and may be used to combat
 CC e.g. glioma, melanoma or carcinoma.
 CC See also Q27040-1.
 SQ Sequence 501 BP; 127 A; 146 C; 124 G; 104 T;

Initial Score = 256 Optimized Score = 269 Significance = 17.51
 Residue Identity = 75% Matches = 275 Mismatches = 82
 Gaps = 6 Conservative Substitutions = 0

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                                X      10      20
                                GTCAAACTGCAGCAGTCTGGGG
                                ||| | |||| | | |||||
GCTATATCATCCTCTTTTTGGTAGCAACAGCTACAGATGTCCACTCCCAGGTCCAGCTGCAACAACCTGGGG
   50      60      70      80      90      100     110

   30      40      50      60      70      80      90
CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTA-AAGACACC
| | | | ||||| | ||| | ||||| ||||| ||||| | | | | | | | | | | | | | | | |
CTGAACTGGTGAAGCCTGGGGCTTCAAGTGAAGTTGTCCTGCAAGGCTTCCGGCTACACCTTACCAGCCA-C
   120     130     140     150     160     170     180

   100     110     120     130     140     150     160
TATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTCGGAGTGGC

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      TGGATGCACTGGGTGAAGCAGAGGGCTGGACAAGGCCTTGAGTGGATCGGAGAGTTTAATCCAGCAACGGC
      190      200      210      220      230      240      250

      170      180      190      200      210      220      230
      GATACTAAATATGACCCGAAGTTCAGGTCAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGG
      ||||| || | ||| ||| || ||||| || || | ||| ||||| |||||
      CGTACTAACTACAATGAGAAATTCAGAGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC
      260      270      280      290      300      310      320

      240      250      260      270      280      290      300
      CTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTG-CAGAC-GGAATGTGGGTATCAA
      ||| ||||| ||||| ||||| ||||| ||||| ||| | ||| || | |||
      ATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCCGTCTATTACTGTGCCAGTCGGGACTATGATTA-CGA
      330      340      350      360      370      380      390

      310      320      330      340      350      X
      CGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
      ||| | || | ||| ||||| ||||| ||||| |||||
      CGGACGGTACT-TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAAAACAACACCCCATC
      400      410      420      430      440      450      460

      GGTCTATCCACTGGATTCTCTAGAGTCGAC
      470      480      490      500

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6. US-07-977-702-1 (1-360)

Q23863 ScFvB18 construct mutant #6.

ID Q23863 standard; DNA; 770 BP.
AC Q23863;
DT 21-MAY-1992 (first entry)
DE ScFvB18 construct mutant #6.
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..770
FT /*tag= a
FT /product= scFvB18
FT mutation 734
FT /*tag= b
FT /note= "c -> t; Thr -> Ile (VL FR4)"
PN W09201047-A.
PD 23-JAN-1992.
PF 10-JUL-1991; G01134.
PR 10-JUL-1990; GB-015198.
PR 19-OCT-1990; GB-022845.
PR 12-NOV-1990; GB-024503.
PR 06-MAR-1991; GB-004744.
PR 15-MAY-1991; GB-010549.
PA (CAMB-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonner TP;
DR MPI; 92-056862/07.
DR P-PSDB; R22587.
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
PS Example 38; Fig 44; 209pp; English.
CC The sequence encodes an antibody scFv fragment directed against 4-
CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
CC against NP were separately amplified and reassembled to form the

CC Construct, which was then ligated into the fd gene III contg. vec-
 CC tor, fdCAT2, derived from fdTPs/Xh. (See Q21095). The clone having
 CC the scFvB18 sequence (see Q21100) fused in frame to gene III was
 CC designated fdCAT2scFvB18. Alternatively the fragment was cloned
 CC into fdDOGkan (fdCAT2 with the tet gene replaced by a kanamycin
 CC resistance gene) to give fdDOGkanscFvB18, or into the phagenid
 CC pHEN1 to create pHEN1-scFvB18. The constructs were used to test
 CC the effect of using mutator strains to increase the diversity of
 CC the cloned genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and
 CC NR9046mutT1: NR9046mutT1::Tn10 were constructed by P1 transduction.
 CC After 4 rounds of mutation and screening, 40 phage inserts were
 CC sequenced. They each displayed single mutations in 6 different
 CC positions, five being in the light chain region. More than 70% of
 CC the mutations occurred at positions 724 and 725 changing the first
 CC Gly in the J segment (framework 4) to Ser (in 21 cases here) or
 CC Asp (in 3 cases). The mutant shown here (see feature table for
 CC details of the mutation) occurred once. The mutant fragments had
 CC affinities for NP which were comparable to the wild-type scFv
 CC fragment (20nM).
 CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
 CC See also Q21092-100, 103-116, 126-131; Q23463, 465-495, 693-719,
 CC 736-738, and 793-862.

SB Sequence 770 BP; 188 A; 196 C; 214 G; 172 T;

Initial Score = 236 Optimized Score = 280 Significance = 16.05
 Residue Identity = 79% Matches = 288 Mismatches = 65
 Gaps = 11 Conservative Substitutions = 0

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          X      10      20      30      40      50
          GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTC
          ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
TTCTATTCTCACAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTG
    10      20 X      30      40      50      60      70

    60      70      80      90      100     110     120
AAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAA
||| ||||| ||||| ||||| ||| | | | | | ||| ||||| ||||| ||||| ||||| ||||| |||||
AAGCTGTCCTGCAAGGCTTCTGGTACACCTTACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGA
    80      90      100     110     120     130     140

    130     140     150     160     170     180     190
CAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCAGGTC
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAGAGC
    150     160     170     180     190     200     210

    200     210     220     230     240     250     260
AAGGCCACTATTACAGCGGACAGCTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGAC
||||||| | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AAGGCCACACTGACTGTAGACAAACCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC
    220     230     240     250     260     270     280

    270     280     290     300     310     320     330
ACTGCCGTCTACTACTGTGC-AGA-CGGAATGTGG--GTATCAACGGGATATGCTCTGGACTTCTGGGGCCA
||| ||||| || ||||| ||| || | || ||| ||| || || || ||||| ||||| ||||| |||||
TCTGCGGTCTATTATTGTGCAAGATACGACTACGGTAGTAGCTAC----TA--CT-TTGACTACTGGGGCCA
    290     300     310     320     330     340     350

    340     350      X
AGGGACCACGGTCACCGTCTCCTCA
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCCA
    360     370     380     390     400     410     420

```

7. US-07-977-702-1 (1-360)

Q23862 ScFvB18 construct mutant #5.

ID Q23862 standard; DNA; 770 BP.
AC Q23862;
DT 21-MAY-1992 (first entry)
DE ScFvB18 construct mutant #5.
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..770
FT /*tag= a
FT /product= scFvB18
FT mutation 725
FT /*tag= b
FT /note= "g -> a; Gly -> Asp (VL FR4)"
PN W09201047-A.
PD 23-JAN-1992.
PF 10-JUL-1991; G01134.
PR 10-JUL-1990; GB-015198.
PR 19-OCT-1990; GB-022845.
PR 12-NOV-1990; GB-024503.
PR 06-MAR-1991; GB-004744.
PR 15-MAY-1991; GB-010549.
PA (CAMB-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonner TP;
DR WPI; 92-056862/07.
DR P-PSDB; R22586.
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
PS Example 38; Fig 44; 209pp; English.
CC The sequence encodes an antibody scFv fragment directed against 4-
CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
CC against NP were separately amplified and reassembled to form the
CC construct, which was then ligated into the fd gene III contg. vec-
CC tor, fdCAT2, derived from fdTPs/Xh.(See Q21095). The clone having
CC the scFvB18 sequence (see Q21100) fused in frame to gene III was
CC designated fdCAT2scFvB18. Alternatively the fragment was cloned
CC into fdDOGkan (fdCAT2 with the tet gene replaced by a kanamycin
CC resistance gene) to give fdDOGkanscFvB18, or into the phagemid
CC pHEN1 to create pHEN1-scFvB18. The constructs were used to test
CC the effect of using mutator strains to increase the diversity of
CC the cloned genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and
CC NR9046mutT1: NR9046mutT1::Tn10 were constructed by P1 transduction.
CC After 4 rounds of mutation and screening, 40 phage inserts were
CC sequenced. They each displayed single mutations in 6 different
CC positions, five being in the light chain region. More than 70% of
CC the mutations occurred at positions 724 and 725 changing the first
CC Gly in the J segment (framework 4) to Ser (in 21 cases), or Asp (in
CC 3 cases as shown here). The mutant fragments had affinities for
CC NP which were comparable to the wild-type scFv fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also Q21092-100, 103-116, 126-131; Q23463, 465-495, 693-719,
CC 736-738, and 793-863.
SQ Sequence 770 BP; 189 A; 197 C; 213 G; 171 T;

Initial Score = 236 Optimized Score = 280 Significance = 16.05
Residue Identity = 79% Matches = 288 Mismatches = 65

PR 06-MAR-1991; GB-004744.
 PA (CAMB-) CAMBRIDGE ANTIBODY.
 PA (MEDI-) MED RES COUNCIL.
 PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
 PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
 PI Winter GP, Bonner TP;
 DR WPI: 92-056862/07.
 DR P-PSDB; R22585.
 PT Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic
 PT display package.
 PS Example 38; Fig 44; 209pp; English.
 CC The sequence encodes an antibody scFv fragment directed against 4-
 CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
 CC against NP were separately amplified and reassembled to form the
 CC construct, which was then ligated into the fd gene III contg. vec-
 CC tor, fdCAT2, derived from fdTPs/Xh.(See Q21095). The clone having
 CC the scFvB18 sequence (see Q21100) fused in frame to gene III was
 CC designated fdCAT2scFvB18. Alternatively the fragment was cloned
 CC into fdDOGkan (fdCAT2 with the tet gene replaced by a kanamycin
 CC resistance gene) to give fdDOGkanscFvB18, or into the phagemid
 CC pHEN1 to create pHEN1-scFvB18. The constructs were used to test
 CC the effect of using mutator strains to increase the diversity of
 CC the cloned genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and
 CC NR9046mutT1: NR9046mutT1::Tn10 were constructed by P1 transduction.
 CC After 4 rounds of mutation and screening, 40 phage inserts were
 CC sequenced. They each displayed single mutations in 6 different
 CC positions, five being in the light chain region. More than 70% of
 CC the mutations occurred at positions 724 and 725 changing the first
 CC Gly in the J segment (framework 4) to Ser (in 21 cases, as shown
 CC here) or Asp (in 3 cases). The mutant fragments had affinities
 CC for NP which were comparable to the wild-type scFv fragment (20nM).
 CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
 CC See also Q21092-100, 103-116, 126-131; Q23463, 465-495, 693-719,
 CC 736-738, and 793-863.
 SQ Sequence 770 BP; 189 A; 197 C; 213 G; 171 T;

Initial Score = 236 Optimized Score = 280 Significance = 16.05
 Residue Identity = 79% Matches = 288 Mismatches = 65
 Gaps = 11 Conservative Substitutions = 0

```

      X      10      20      30      40      50
      GTCAAAGTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCTCAGTC
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
TTCTATTCTCACAGTGCACAGGTCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTCAGTG
      10      20 X      30      40      50      60      70

      60      70      80      90      100     110     120
AAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAA
||| ||||| ||||| ||||| ||| | | | | | ||||| ||||| ||||| ||||| ||||| |||||
AAGCTGTCCTGCAAGGCTTCTGGTACACCTTACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGA
      80      90      100     110     120     130     140

      130     140     150     160     170     180     190
CAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCCAGTGGCGATACTAAATATGACCCGAAGTTCAGGTC
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTACTAAGTACAATGAGAAGTTCAAGAGC
      150     160     170     180     190     200     210

      200     210     220     230     240     250     260
AAGGCCACTATTACAGCGGACAGCTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGAC
||||| | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AAGGCCACACTGACTGTAGACAAACCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC
      220     230     240     250     260     270     280
  
```


specific binding pairs; replicable genetic display package; ds.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 1..770
 FT /*tag= a
 FT /product= scFvB18
 FT mutation 703
 FT /*tag= b
 FT /note= "t -> g; Tyr -> Asp (VL CDR3)"
 PN W09201047-A.
 PD 23-JAN-1992.
 PF 10-JUL-1991; G01134.
 PR 10-JUL-1990; GB-015198.
 PR 19-OCT-1990; GB-022845.
 PR 12-NOV-1990; GB-024503.
 PR 06-MAR-1991; GB-004744.
 PR 15-MAY-1991; GB-010549.
 PA (CAMB-) CAMBRIDGE ANTIBODY.
 PA (MEDI-) MED RES COUNCIL.
 PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
 PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
 PI Winter GP, Bonner TP;
 DR WPI; 92-056862/07.
 DR P-PSDB; R22583.
 PT Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic
 PT display package.
 PS Example 38; Fig 44; 209pp; English.
 CC The sequence encodes an antibody scFv fragment directed against 4-
 CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
 CC against NP were separately amplified and reassembled to form the
 CC construct, which was then ligated into the fd gene III contg. vec-
 CC tor, fdCAT2, derived from fdTPs/Xh. (See Q21095). The clone having
 CC the scFvB18 sequence (see Q21100) fused in frame to gene III was
 CC designated fdCAT2scFvB18. Alternatively the fragment was cloned
 CC into fdDOGkan (fdCAT2 with the tet gene replaced by a kanamycin
 CC resistance gene) to give fdDOGkanscFvB18, or into the phagemid
 CC pHEN1 to create pHEN1-scFvB18. The constructs were used to test
 CC the effect of using mutator strains to increase the diversity of
 CC the cloned genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and
 CC NR9046mutT1: NR9046mutT1::Tn10 were constructed by P1 transduction.
 CC After 4 rounds of mutation and screening, 40 phage inserts were
 CC sequenced. They each displayed single mutations in 6 different
 CC positions, five being in the light chain region. More than 70% of
 CC the mutations occurred at positions 724 and 725 changing the first
 CC Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp (in
 CC 3 cases). The mutant shown here (see feature table for details of
 CC mutation) occurred once. The mutation shown on the fig., of t -> c
 CC would result in the Tyr being replaced by His, contrary to the data
 CC in Table 9 of the specification which indicates that the substn. is
 CC with Asp (i.e. t -> g). The mutant fragments had affinities for NP
 CC which were comparable to the wild-type scFv fragment (20nM).
 CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
 CC See also Q21092-100, 103-116, 126-131; Q23463, 465-495, 693-719,
 CC 736-738, and 793-863.
 SQ Sequence 770 BP; 188 A; 197 C; 215 G; 170 T;

Initial Score = 236 Optimized Score = 280 Significance = 16.05
 Residue Identity = 79% Matches = 288 Mismatches = 65
 Gaps = 11 Conservative Substitutions = 0

	X	10	20	30	40	50
	GTCAAAGCTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTC					
TTCTATTCTCAGAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTG	10	20 X	30	40	50	60 70

FT /note= "c -> t; Thr -> Ile (VL FR4); 023863"
 PN W09201047-A.
 PD 23-JAN-1992.
 PF 10-JUL-1991; G01134.
 PR 10-JUL-1990; GB-015198.
 PR 19-OCT-1990; GB-022845.
 PR 12-NOV-1990; GB-024503.
 PR 06-MAR-1991; GB-004744.
 PR 15-MAY-1991; GB-010549.
 PA (CAMB-) CAMBRIDGE ANTIBODY.
 PA (MEDI-) MED RES COUNCIL.
 PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
 PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
 PI Winter GP, Bonner TP;
 DR WPI: 92-056862/07.
 DR P-PSDB; R22568.
 PT Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic
 PT display package.
 PS Example 38; Fig 44; 209pp; English.
 CC The sequence encodes an antibody scFv fragment directed against 4-
 CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
 CC against NP were separately amplified and reassembled to form the
 CC construct, which was then ligated into the fd gene III contg. vec-
 CC tor, fdCAT2, derived from fdTPs/Xh. (See 021095). The clone having
 CC the scFvB18 sequence fused in frame to gene III was designated
 CC fdCAT2scFvB18. Alternatively the fragment was cloned into fdDOGkan
 CC (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
 CC to give fdDOGkanscFvB18, or into the phagemid pHEN1 to create pHEN1-
 CC scFvB18. The constructs were used to test the effect of using muta-
 CC tor strains to increase the diversity of the cloned genes. The
 CC strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1: NR9046
 CC mutT1::Tn10 were constructed by P1 transduction. After 4 rounds of
 CC mutation and screening, 40 phage inserts were sequenced. They each
 CC displayed single mutations in 6 different positions, five being in
 CC the light chain region. More than 70% of the mutations occurred at
 CC positions 724 and 725 changing the first Gly in the J segment
 CC (framework 4) to Ser (in 21 cases) or Asp (in 3 cases). The
 CC mutant fragments had affinities for NP which were comparable to the
 CC wild-type scFv fragment (20nM).
 CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
 CC See also 021092-99, 103-116, 126-131; 023463, 465-495, 693-719,
 CC 736-738, and 793-863.
 SQ Sequence 770 BP; 188 A; 197 C; 214 G; 171 T;

Initial Score = 236 Optimized Score = 280 Significance = 16.05
 Residue Identity = 79% Matches = 288 Mismatches = 65
 Gaps = 11 Conservative Substitutions = 0

```

          X      10      20      30      40      50
          GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCTCAGTC
          ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
TTCTATTCTCACAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAAGT
      10      20 X      30      40      50      60      70

      60      70      80      90      100     110     120
AAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAGACACCTATATGCACTGGGTGAAGCAGAGGCTGAA
||| ||||| ||||| ||||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
AAGCTGTCCTGCAAGGCTTCTGGCTACACCTTACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCTTGA
      80      90      100     110     120     130     140

      130     140     150     160     170     180     190
CAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCCAGTGGCGATACTAAATATGACCCGAAGTTCAGGTC
| |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAGAGC

```

```

150      160      170      180      190      200      210
200      210      220      230      240      250      260
AAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGAC
||||||| | | | |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AAGGCCACACTGACTGTAGACAAACCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC
220      230      240      250      260      270      280

270      280      290      300      310      320      330
ACTGCCGTCTACTACTGTGC-AGA-CGGAATGTGG--GTATCAACGGGATATGCTCTGGACTTCTGGGGCCA
|||| | |||| | | |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
TCTGCCGTCTATTATTGTGCAAGATACGACTACGGTAGTAGCTAC----TA--CT-TTGACTACTGGGGCCA
290      300      310      320      330      340      350

340      350      X
AGGGACCACGGTCACCGTCTCCTCA
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCCA
360      370      380      390      400      410      420

```

GGC

12. US-07-977-702-1 (1-360)

Q23858 ScFvB18 construct mutant #1.

ID Q23858 standard; DNA; 770 BP.
AC Q23858;
DT 21-MAY-1992 (first entry)
DE ScFvB18 construct mutant #1.
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..770
FT /*tag= a
FT /product= scFvB18
FT mutation 308
FT /*tag= b
FT /note= "c -> t; Ala -> Val (VH FR3)"
PN M09201047-A.
PD 23-JAN-1992.
PF 10-JUL-1991; G01134.
PR 10-JUL-1990; GB-015198.
PR 19-OCT-1990; GB-022845.
PR 12-NOV-1990; GB-024503.
PR 06-MAR-1991; GB-004744.
PR 15-MAY-1991; GB-010549.
PA (CAMB-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnert TP;
DR MPI; 92-056862/07.
DR P-PSDB; R22582.
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
PS Example 38; Fig 44; 209pp; English.
CC The sequence encodes an antibody scFv fragment directed against 4-
CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
CC against NP were separately amplified and reassembled to form the
CC construct, which was then ligated into the fd gene III contg. vec-
CC tor, fdCAT2, derived from fdTPs/Xh.(See Q21095). The clone having

CC the scFvB18 sequence (see Q21100) fused in frame to gene III was
 CC designated fdCAT2scFvB18. Alternatively the fragment was cloned
 CC into fdDOGkan (fdCAT2 with the tet gene replaced by a kanamycin
 CC resistance gene) to give fdDOGkanscFvB18, or into the phagenid
 CC pHEN1 to create pHEN1-scFvB18. The constructs were used to test
 CC the effect of using mutator strains to increase the diversity of
 CC the cloned genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and
 CC NR9046mutT1: NR9046mutT1::Tn10 were constructed by P1 transduction.
 CC After 4 rounds of mutation and screening, 40 phage inserts were
 CC sequenced. They each displayed single mutations in 6 different
 CC positions, five being in the light chain region. More than 70% of
 CC the mutations occurred at positions 724 and 725 changing the first
 CC Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp (in
 CC 3 cases). The mutant shown here (see feature table for details of
 CC mutation) occurred three times. The mutant fragments had affinities
 CC for NP which were comparable to the wild-type scFv fragment (20nM).
 CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
 CC See also Q21092-100, 103-116, 126-131; Q23463, 465-495, 693-719,
 CC 736-738, and 793-863.
 SQ Sequence 770 BP; 188 A; 196 C; 214 G; 172 T;

Initial Score = 234 Optimized Score = 279 Significance = 15.90
 Residue Identity = 78% Matches = 287 Mismatches = 66
 Gaps = 11 Conservative Substitutions = 0

```

          X      10      20      30      40      50
          GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTC
          ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
TTCTATTCTCACAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTG
      10      20 X      30      40      50      60      70

      60      70      80      90      100     110     120
AAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAA
||| ||||| ||||| ||||| ||| | | | | | ||| ||||| ||||| ||||| ||||| |||||
AAGCTGTCCTGCAAGGCTTCTGGCTACACCTTACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGA
      80      90      100     110     120     130     140

      130     140     150     160     170     180     190
CAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCCAGTGGCGATACTAAATATGACCCGAAGTTCAGGTC
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAGAGC
      150     160     170     180     190     200     210

      200     210     220     230     240     250     260
AAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGAC
||||| ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AAGGCCCACTGACTGTAGACAAACCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC
      220     230     240     250     260     270     280

      270     280     290     300     310     320     330
ACTGCCGTCTACTACTGTG-CAGA-CGGAATGTGG--GTATCAACGGGATATGCTCTGGACTTCTGGGGCCA
||| ||||| || ||||| ||| ||| ||| ||| ||| ||| ||| ||||| ||||| |||||
TCTGCGGTCTATTATTGTGTAAGATACGACTACGGTAGTAGCTAC----TA--CT-TTGACTACTGGGGCCA
      290     300     310     320     330     340     350

      340     350      X
AGGGACCACGGTCACCGTCTCCTCA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCCA
      360     370     380     390     400     410     420

```

GGC

ID Q15164 standard; DNA; 458 BP.
AC Q15164;
DT 16-MAR-1992 (first entry)
DE VH186 region of anti-nitrophenylacetyl heavy chain Ab gene.
KW mouse; murine; antibody; heavy chain; variable region;
KW polymerase chain reaction; ss.
OS Mus musculus.
PN J03247283-A.
PD 05-NOV-1991.
PF 29-DEC-1989; 340628.
PR 29-DEC-1989; JP-340628.
PA (MATU) MATSUSHITA ELEC IND KK.
DR MPI; 91-366330/50.
PT DNA binding to termini of anti-nitrophenyl:acetyl antibody gene
PT - allows specific amplification of variable region in gene by PCR
PS Disclosure; Page 2; 3pp; Japanese.
CC This sequence corresponds to the region of the heavy chain variable
CC region of the murine anti-nitrophenylacetyl IgG antibody which is
CC amplified by PCR primers HA and HS.
CC See Q15159-Q15163.
SQ Sequence 458 BP; 112 A; 124 C; 120 G; 102 T;

Initial Score = 233 Optimized Score = 277 Significance = 15.83
Residue Identity = 78% Matches = 283 Mismatches = 72
Gaps = 7 Conservative Substitutions = 0

```

                                     X      10      20
                                     GTCAAACTGCAGCAGTCTGGGG
                                     ||| ||||| ||||| |||||
GCTGTATCATGCTCTTCTTGGCAGCAACAGCTACAGGTGTCCACTCCCAGGTCCAAGTGCAGCAGCCTGGGG
  20      30      40      50      60      70      80

  30      40      50      60      70      80      90
CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTGAGCTTGTGAAGCCTGGGGCTTCAAGTGAAGCTGTCTGCAAGGCTTCTGGCTACACCTTACCAGCTACT
  90     100     110     120     130     140     150

 100     110     120     130     140     150     160
ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GGATGCACTGGGTGAAGCAGAGGCTGGACGAGGCTTGAAGTGGATTGGAAGGATTGATCCTAATAGTGGTG
 160     170     180     190     200     210     220

 170     180     190     200     210     220     230
ATACTAAATATGACCCGAAGTTCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GTACTAAGTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCCTCCAGCACAGCCTACA
 230     240     250     260     270     280     290

 240     250     260     270     280     290     300     310
TGCAGCTCAGCAGCCTGACATCTGAGGACTGCGGTCTACTACTGTGCAGACGGAATGTGGGTATCAACGG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TGCAGCTCAGCAGCCTGACATCTGAGGACTGCGGTCTATTATTGTGCA---AGA-TACGATTA-CTACGG
 300     310     320     330     340     350     360

  320     330     340     350      X
GATATGCT-CT-GGACTTCTGGGGCAAGGGACCACGGTCACCGTCTCCTCA
| ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TAGTAGCTACTTTGACTACTGGGGCAAGGCACCACTCTCACAGTCTCCTCAGCCAAAACAACAGCCCCATC
 370     380     390     400     410     420     430

GGTCTATCCACTGGCCCTGT
 440     450
```

14. US-07-977-702-1 (1-360)
006227 VH domain of antibody C against tumour-associated

ID 006227 standard; DNA; 345 BP.
AC 006227;
DT 22-JAN-1991 (first entry)
DE VH domain of antibody C against tumour-associated antigens.
KW Tumour-associated antigen; murine monoclonal antibody C;
KW pancreatic carcinoma; metastases; diagnosis; ss.
OS Mus musculus.
PN EP-388914-A.
PD 26-SEP-1990.
PF 21-MAR-1990; 105322.
PR 24-MAR-1989; DE-909799.
PA (BEHW) BEHRINGWERKE AG.
PI Bosslet K, Seemann G, Sedlacek HH;
DR MPI; 90-291873/39.
DR P-PSDB; R07320.
PT Monoclonal antibodies to tumour associated antigens - used for
PT diagnosis of malignant tumours etc.
PS Disclosure; Page 13; 18pp; German.
CC Antibody C is produced as described in EP-141079 and binds to
CC pancreatic carcinoma primary tumours and metastases.
CC They are useful in tumour diagnosis and therapy.
CC See also 006228 for VK of MAb C, 007312-15 for MAb A and B and
CC 006229-30 for MAb D.
SQ Sequence 345 BP; 87 A; 87 C; 93 G; 78 T;

Initial Score = 229 Optimized Score = 245 Significance = 15.53
Residue Identity = 71% Matches = 255 Mismatches = 86
Gaps = 15 Conservative Substitutions = 0

```

X      10      20      30      40      50      60
GTCAAAGTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGCTCCTGCACAGCT
||| ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CAGGTCCAAGTGCAGCAGTCTGGAGCTGAGCTGGTAAAGCCTGGGGCTTCAAGTGAAGATGCTCCTGCAAGGCT
X      10      20      30      40      50      60      70
```

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70      80      90     100     110     120     130     140
TCTGGCTTCAACATT-AAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGAT
||||| ||| ||||| || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TCTGGATAC-ACATTCACTTACTATGTTATTCAGTGGGTGAAGCAGAGGCCTGGGGCAGGGCCTTGAAGTGGAT
80      90     100     110     120     130     140
```

```

150     160     170     180     190     200     210
TGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCAGGTCAGGCCACTATTACAGC
|||| ||| ||||| || ||| ||||| || ||| ||||| || ||| ||||| || ||| ||||| || |||
TGGATACATTATCCTTACAATGCTGGTACTGAGTACAATGAGAAGTTCAAAGGCAAGGCCACACTGACTTC
150     160     170     180     190     200     210
```

```

220     230     240     250     260     270     280
GGACAGTCTCTCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTG
|||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AGACAAATCCTCCAGCACAGCCTACATGGAGCTCAGCAGCCTGACCTCTGAGGACTCTGCCGTCTATTACTG
220     230     240     250     260     270     280
```

```

290     300     310     320     330     340     350   X
TGCAGACGGAATGTGGGTATCAACGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTC
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
TTCA-ATGGGACGAGGGGGT-----GACTA--CTGGGGCC--AAGGGACCACGG--TCACCGTCTCC-TCA
290     300     310     320     330     340     X
```

360
CTCA

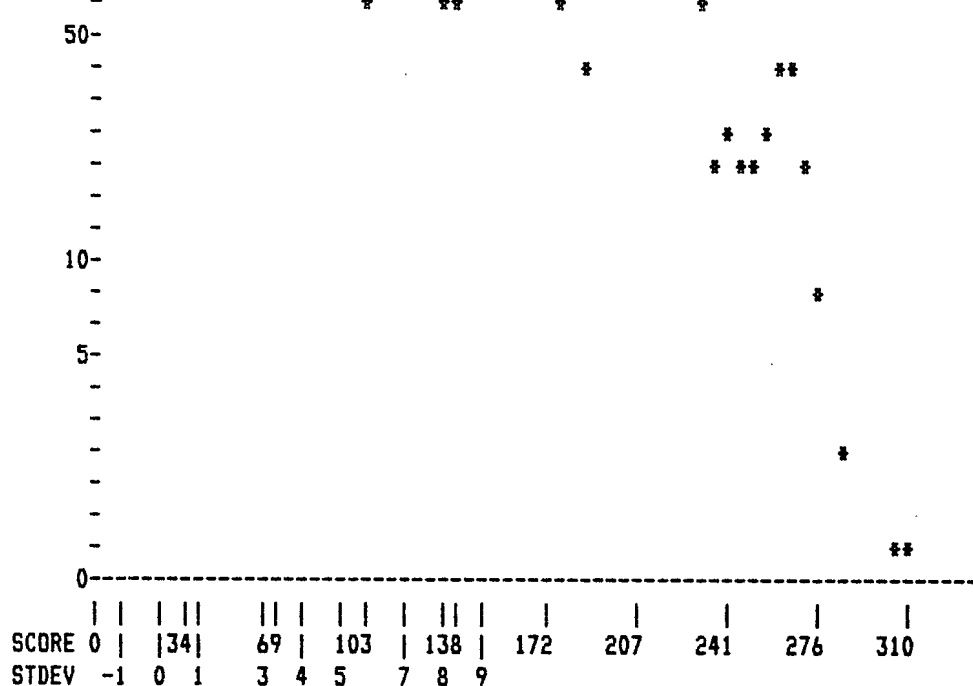
N91482 Genomic to cDNA junction (V47 to VB1-8) DNA

Initial Score = 228 Optimized Score = 269 Significance = 15.46
Residue Identity = 77% Matches = 275 Mismatches = 71
Gaps = 7 Conservative Substitutions = 0

290 300 310 320 330 340 350
GACGGAATGTGGGTATCAACGGGATATGCT-CT-GGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCT
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
---AGA-TACGATTA-CTACGGTAGTAGCTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCT
280 290 300 310 320 330 340

360
CA
II
CAG
X

[illegible]



PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	1.00	Window size	32
Gap size penalty	0.33		
Cutoff score	0		
Randomization group	0		

Initial scores to save	40	Alignments to save	15
Optimized scores to save	0	Display context	50

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	28	28	13.45

Times:	CPU	Total Elapsed
	00:30:37.12	01:03:42.00

Number of residues: 150464018
 Number of sequences searched: 125798
 Number of scores above cutoff: 4369

- Cut-off raised to 22.
- Cut-off raised to 26.
- Cut-off raised to 30.
- Cut-off raised to 33.
- Cut-off raised to 36.
- Cut-off raised to 39.
- Cut-off raised to 41.
- Cut-off raised to 44.
- Cut-off raised to 46.
- Cut-off raised to 49.
- Cut-off raised to 53.
- Cut-off raised to 58.
- Cut-off raised to 64.

The scores below are sorted by initial score.
 Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Opt.		Sig.	Frame
			Score	Score		
**** 20 standard deviations above mean ****						
1. MMIGGNP2	Mouse mRNA for idiotypic anti	420	310	318	20.97	0
2. MMCEAHCH	M.musculus gene for anti-CEA	861	309	316	20.89	0
3. MUSIGHNPA	Mouse Ig active H-chain mRNA,	421	305	318	20.60	0
**** 18 standard deviations above mean ****						
4. MUSIGHNP	Mouse Ig active H-chain mRNA,	414	281	314	18.81	0
5. MMIGGNP1	Mouse mRNA for idiotypic anti	414	281	314	18.81	0
6. MMV20292B	M.musculus mRNA for VH-gen se	363	276	282	18.44	0
7. S114902	immunoglobulin heavy chain (n	452	276	281	18.44	0
8. MMIGVDJAA	M.musculus immunoglobulin hea	452	276	281	18.44	0
9. MUSIGHNPG	Mouse Ig active H-chain mRNA,	414	273	309	18.22	0
10. MMIGGNP8	Mouse mRNA for idiotypic anti	414	273	307	18.22	0
11. MUSIGHNPB	Mouse Ig active H-chain mRNA,	414	272	307	18.14	0
12. MMIGGNP3	Mouse mRNA for idiotypic anti	414	272	308	18.14	0
13. MMIGG1HCV	M.musculus rearranged mRNA fo	351	271	316	18.07	0
14. MUSIGMU4G	Mouse monoclonal antiidiotypi	354	271	307	18.07	0
15. MUSIGHBB	Mouse Ig active mu-chain VDJ-	390	271	326	18.07	0
16. MUSIGHBH	Mouse Ig active H-chain: anti	501	271	324	18.07	0
17. MMIGVK1	Mouse mRNA for anti-GAT VH an	501	271	324	18.07	0
18. MUSIGHXO	Mouse Ig germline H-chain gen	970	271	305	18.07	0
19. MMIG10VH	Mouse (GAT-specific) subgroup	970	271	305	18.07	0
20. MMIGHVXA	Mouse (hybridoma 3A112) immun	1069	271	277	18.07	0
21. MUSIGHVXA	Mouse (hybridoma 3A112) immun	1069	271	277	18.07	0
**** 17 standard deviations above mean ****						
22. MMV20311	M.musculus mRNA for VH-gen se	363	270	279	17.99	0
23. MUSIGHADE	Mouse Ig rearranged H-chain g	404	270	275	17.99	0
24. MUSIGHEA	Mouse Ig mu-chain active V-re	444	269	322	17.92	0
25. MUSIGHDZ	Mouse Ig mu-chain active V-re	444	269	322	17.92	0
26. MUSIGHNPH	Mouse Ig active H-chain mRNA,	417	268	321	17.85	0
27. MUSIGHBC	Mouse Ig active H-chain a-NP	511	268	321	17.85	0
28. MUSIGHZTA	Mouse Ig germline H-chain gen	294	267	272	17.77	0
29. MUSIGHZP	Mouse Ig germline H-chain gen	294	266	271	17.70	0
30. MUSIGHAEM	Mouse Ig heavy-chain mRNA V r	328	266	288	17.70	0
31. MUSIGB1H1	Mouse mRNA for immunoglobulin	1544	266	271	17.70	0
32. MMIGB1H1	Mouse mRNA for immunoglobulin	1544	266	271	17.70	0
33. MUSIGHZQ	Mouse Ig germline H-chain gen	291	265	268	17.62	0
34. MUSIGHZN	Mouse Ig germline H-chain gen	291	265	267	17.62	0
35. MUSIGHDF	Mouse Ig active mu-chain V-re	363	265	271	17.62	0
36. MMIGNP4	Mouse mRNA for idiotypic anti	411	265	310	17.62	0
37. MUSIGHNPE	Mouse Ig active H-chain mRNA,	417	265	312	17.62	0
38. MMIGGNP6	Mouse mRNA for idiotypic anti	417	265	312	17.62	0
39. MMIGWM65B	M.musculus WM65 immunoglobuli	536	265	317	17.62	0
40. MMIGHVXZ	Mouse (hybridoma H1-39) immun	1068	265	273	17.62	0

1. US-07-977-702-1 (1-360)

MMIGGNP2 Mouse mRNA for idiotypic anti-NP IgG(1) heavy chain

LOCUS MMIGGNP2 420 bp RNA ROD 07-MAY-1992

DEFINITION Mouse mRNA for idiotypic anti-NP IgG(1) heavy chain V-D-J (hybridoma 18.1.16)

ACCESSION X02563 M12744

KEYWORDS gamma-immunoglobulin; Ig D-segment; Ig heavy chain; immunoglobulin; joining region; signal peptide; variable region.

SOURCE mouse

ORGANISM Mus musculus

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 420)

AUTHORS Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and Imanishi-Kari,T.
 TITLE Heavy chain variable region: Multiple gene segments encode anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
 JOURNAL J. Exp. Med. 161, 1272-1292 (1985)
 STANDARD full automatic
 COMMENT *source: strain=Balb/c;

Serological analysis of hybridoma proteins resulting from the immune response to the hapten NP reveals NP(a) idiotypes expressed by Balb/C mice and NP(b) idiotypes expressed by C57 BL/6 mice. The NP(b) family of antibodies consists of 6 subgroups (I-VI) with I-IV sharing more determinants than V and VI which appear quite distinct.

FEATURES Location/Qualifiers
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 mat_peptide join(58..351,352..375,376..420)
 /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
 misc_feature 58..351
 /note="variable region (aa 1-98)"
 misc_feature 148..162
 /note="CDR I"
 misc_feature 205..255
 /note="CDR II"
 misc_feature 352..375
 /note="D-region (aa 99-106)"
 misc_feature 376..>420
 /note="J-region (aa 107-121)"
 CDS join(1..351,352..375,376..420)
 /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
 /codon_start=1
 /translation="MKCSWVMFFLMAVVTGVNSEVQLQGSGAELVKPGASVKLSCTAS
 GFNIKDTYMHVVKQRPEQGLEWIGRIDPANGNTKYDPKFQGGKATITADTSSNTAYLQL
 SSLTSEDTA VYYCARYLYYYGSSDFDYWGQGTTLTVSS"
 BASE COUNT 107 a 106 c 110 g 97 t
 ORIGIN

Initial Score = 310 Optimized Score = 318 Significance = 20.97
 Residue Identity = 88% Matches = 323 Mismatches = 34
 Gaps = 6 Conservative Substitutions = 0

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                                     GTCAAACTGCAGCAGTCTGGGG
                                     || | |||||
GCTGGGTTATGTTCTTCTCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGTTTCAGCTGCAGCAGTCTGGGG
    20      30      40      50      60      70      80

    30      40      50      60      70      80      90
CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
|||||
CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCTGCACGGCTTCTGGCTTCAACATTAAAGACACCT
    90      100      110      120      130      140      150

    100      110      120      130      140      150      160
ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
|||||
ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
    160      170      180      190      200      210      220

    170      180      190      200      210      220      230
ATACTAAATATGACCCGAAGTTCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
|||||
ATACTAAATATGACCCGAAGTTCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
    230      240      250      260      270      280      290

    240      250      260      270      280      290      300
  
```

TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGCTCTACTACTGTGC-AGACGGAAATGTGGGTATCAACG
 |||||
 TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGCTCTACTACTGTGCTAGA---TACCTCTATTACTACG
 300 310 320 330 340 350 360

310 320 330 340 350 X
 GGA-TA-TGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
 |||||
 GTAGTAGCGACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
 370 380 390 400 410 420

2. US-07-977-702-1 (1-360)

MMCEAHCH M.musculus gene for anti-CEA mAb T84.66 heavy chain

LOCUS MMCEAHCH 861 bp DNA ROD 03-DEC-1992
 DEFINITION M.musculus gene for anti-CEA mAb T84.66 heavy chain V-region
 ACCESSION X52769
 KEYWORDS CEA; heavy chain; tumor-associated antigen.
 SOURCE mouse
 ORGANISM Mus musculus
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 861)
 AUTHORS Neumaier, M., Shively, L., Chen, F.S., Gaida, F.J., Ilgen, C.,
 Paxton, R.J., Shively, J.E. and Riggs, A.D.
 TITLE Cloning of the genes for T86.66, an antibody that has a high
 specificity and affinity for carcinoembryonic antigen, and
 expression of chimeric human/mouse T84.66 genes in myeloma and
 Chinese hamster ovary cells
 JOURNAL Cancer Res. 50, 2128-2134 (1990)
 STANDARD full automatic
 FEATURES Location/Qualifiers
 promoter 109..118
 promoter 121..127
 promoter 160..166
 promoter 169..176
 exon 272..317
 /number=1
 exon 396..770
 /number=2
 intron 318..395
 /number=1
 CDS join(272..317,396..770)
 /partial
 /note="heavy chain"
 /product="anti-CEA mAb T84.66"
 /codon_start=1
 /translation="MKCSWVIFFLMAVVTGVNSEVQLQDSGAELVEPGASVKLSCTAS
 GFNIKDTYMHVWKQRPEQGLEWIGRIDPANGNSKYVPKFQKATITADTSSNTAYLQL
 TSLTSEDYAVYYCAPFGYVVS DYAMAYWGQGTSTVTVSS"
 BASE COUNT 213 a 208 c 203 g 237 t
 ORIGIN

Initial Score = 309 Optimized Score = 316 Significance = 20.89
 Residue Identity = 88% Matches = 322 Mismatches = 33
 Gaps = 10 Conservative Substitutions = 0

X 10 20
 GTCAAAGTGCAGCAGTCTGGGG
 |||
 GTGACAGTGGCAATCACTTTGCCCTTTCTTCTACAGGGGTCAATTGAGAGTTGAGCTGCAGCAGTCTGGGG
 360 370 380 390 400 410 420 430
 30 40 50 60 70 80 90
 CAGAGCTTGTAAGCCAGGGGCTCAGTCAAGTTGCTCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT

```

|||||
CAGAGCTTGTGGAGCCAGGGGCTCAGTCAAGTTGTCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
440      450      460      470      480      490      500

100      110      120      130      140      150      160
ATATGCACTGGGTGAAGCAGAGGCCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
|||||
ATATGCACTGGGTGAAGCAGAGGCCCTGAACAGGGCCTGGAATGGATTGGAAGGATTGATCCTGCGAATGGTA
510      520      530      540      550      560      570

170      180      190      200      210      220      230
ATACTAAATATGACCCGAAGTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATAGTAAATATGTCCCGAAGTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
580      590      600      610      620      630      640

240      250      260      270      280      290      300
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGGAATGTGGGTATCAACG-
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TGCAGCTCACCAGCCTGACATCTGAGGACACTGCCGTCTATTATTGTGC-TCCG---TTTGGTTA-CTACGT
650      660      670      680      690      700      710

310      320      330      340      350      X
----GGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
| ||||| ||| || ||||| ||||| ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
GTCTGACTATGCTATGGCCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGGTAAGAATGGCCTCTC
720      730      740      750      760      770      780

CAGGTCTTTATTTTAACTTTGTATGGACTTT
790      800      810

```

3. US-07-977-702-1 (1-360)

MUSIGHNPA Mouse Ig active H-chain mRNA, V-region (VDJ) from

LOCUS MUSIGHNPA 421 bp ss-mRNA ROD 01-SEP-1988
 DEFINITION Mouse Ig active H-chain mRNA, V-region (VDJ) from anti-NP hybridoma 18.1.16.
 ACCESSION M12744
 KEYWORDS immunoglobulin; immunoglobulin heavy chain; variable region.
 SOURCE Mouse (BALB/c) hybridoma 18.1.16, cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
 Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 421)
 AUTHORS Boersch-Supan, M.E., Agarwal, S., White-Scharf, M.E. and
 Imanishi-Kari, T.
 TITLE Heavy chain variable region Multiple gene segments encode
 anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
 JOURNAL J. Exp. Med. 161, 1272-1292 (1985)
 STANDARD full automatic
 FEATURES Location/Qualifiers
 sig_peptide 1..57
 /codon_start=1
 /note="Ig H-chain V-region signal peptide"
 mat_peptide 58..421
 /codon_start=1
 /note="Ig H-chain V-region"
 misc_recomb 351..352
 /note="V-region end/D-region start"
 misc_recomb 375..376
 /note="D-region end/J-region start"
 CDS 1..421
 /note="Ig H-chain; (VDJ-region) precursor"
 /codon_start=1
 /translation="MKCSWVMFFLMAVVTGVNSEVQLQSGAELVKPGASVKLSCTAS"

GFNIRDYTHHWKGRPEGLWIGRIDPANGNIRYDPRFQGRATITADTSSNTAYLQL
 SSLTSEDYAVYYCARYLYYYGSSYFDYWGQGTTLTVSLX"

BASE COUNT 107 a 106 c 110 g 98 t
 ORIGIN Chromosome 12.

Initial Score = 305 Optimized Score = 318 Significance = 20.60
 Residue Identity = 89% Matches = 324 Mismatches = 33
 Gaps = 7 Conservative Substitutions = 0

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                                GTCAAAGTGCAGCAGTCTGGGG
                                || | ||||| ||||| |||||
GCTGGGTTATGTTCTTCTCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTGAGTGCAGCAGTCTGGGG
   20       30       40       50       60       70       80

   30       40       50       60       70       80       90
CAGAGCTTGTGAAGCCAGGGGCCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CAGAGCTTGTGAAGCCAGGGGCCCTCAGTCAAGTTGTCCTGCACGGCTTCTGGCTTCAACATTAAAGACACCT
   90      100      110      120      130      140      150

  100      110      120      130      140      150      160
ATATGCACTGGGTGAAGCAGAGGCCCTGAACAGGGCCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATATGCACTGGGTGAAGCAGAGGCCCTGAACAGGGCCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
  160      170      180      190      200      210      220

  170      180      190      200      210      220      230
ATACTAAATATGACCCGAAGTTCAGGTCAAGGCCACTATTACAGCGGACACGTCTCCAACACAGCCTGGC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATACTAAATATGACCCGAAGTTCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
  230      240      250      260      270      280      290

  240      250      260      270      280      290      300
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGC-AGACGGAATGTGGGTATCAACG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTAGA---TACCTCTATTACTACG
  300      310      320      330      340      350      360

  310      320      330      340      350      X
GGATATGCT-CT-GGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTC-CTCA
|| | ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GTAGTAGCTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCGCTCA
  370      380      390      400      410      420

```

4. US-07-977-702-1 (1-360)

MUSIGHNP Mouse Ig active H-chain mRNA, V-region (VDJ) from

LOCUS MUSIGHNP 414 bp ss-mRNA ROD 01-SEP-1988
 DEFINITION Mouse Ig active H-chain mRNA, V-region (VDJ) from anti-NP hybridoma 20.1.43.
 ACCESSION M12176
 KEYWORDS immunoglobulin; immunoglobulin heavy chain; variable region.
 SOURCE Mouse (BALB/c) hybridoma 20.1.43, cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
 Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS Boersch-Supan, M.E., Agarwal, S., White-Scharf, M.E. and Inanishi-Kari, T.
 TITLE Heavy chain variable region Multiple gene segments encode anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
 JOURNAL J. Exp. Med. 161, 1272-1292 (1985)
 STANDARD full automatic
 FEATURES Location/Qualifiers

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sig_peptide 1..57
              /codon_start=1
              /note="Ig H-chain V-region signal peptide"
mat_peptide  58..414
              /codon_start=1
              /note="Ig H-chain V-region"
misc_recomb  351..352
              /note="V-region end/D-region start"
misc_recomb  366..367
              /note="D-region end/J-region start"
CDS          1..414
              /note="Ig H-chain; (VDJ-region) precursor"
              /codon_start=1
              /translation="MKCSWVMFFLMAVVTGVNSEVQLQSGAELVRPGASVKLSCTAS
              GFNIKDTYMHVVKQRPEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQL
              SSLTSEDTA VYYCASYRYERAWFAYWGQGLTVTSA"
BASE COUNT   101 a    98 c    118 g    97 t
ORIGIN       Chromosome 12.

```

```

Initial Score   =   281   Optimized Score   =   314   Significance = 18.81
Residue Identity =   88%   Matches           =   321   Mismatches   =   31
Gaps            =    10   Conservative Substitutions   =    0

```

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                                X      10      20
                                GTCAAACTGCAGCAGTCTGGGG
                                || | |||||
GCTGGGTTATGTTCTTCTCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTAGCTGCAGCAGTCTGGGG
    20      30      40      50      60      70      80

    30      40      50      60      70      80      90
CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CAGAGCTTGTGAGGCCAGGGGCTCAGTCAAGTTGTCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
    90     100     110     120     130     140     150

    100     110     120     130     140     150     160
ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
    160     170     180     190     200     210     220

    170     180     190     200     210     220     230
ATACTAAATATGACCCGAAGTTCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATACTAAATATGACCCGAAGTTCAGGGCAAGGCCACTATAACAGCAGACACATCTCCAACACAGCCTACC
    230     240     250     260     270     280     290

    240     250     260     270     280     290     300
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGC-AGACGGAATGTGGGTATCAACG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTAG-----TTATAGGTA-CGAGA
    300     310     320     330     340     350     360

    310     320     330     340     350     360
GGATATGCTCTGGACTT-CTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
|| || || || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GGGCTGTTG--CTTACTGGGGCCAAGGACTCTGGTCACTGTCTCTGCA
    370     380     390     400     410   X

```

5. US-07-977-702-1 (1-360)

MMIGGNP1 Mouse mRNA for idiotypic anti-NP IgG(1) heavy chain

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LOCUS      MMIGGNP1      414 bp      RNA      ROD      07-MAY-1992
DEFINITION Mouse mRNA for idiotypic anti-NP IgG(1) heavy chain V-J (hybridoma
20.1.43)

```

ACCESSION X02362 M12176
 KEYWORDS gamma-immunoglobulin; Ig D-segment; Ig heavy chain; immunoglobulin; joining region; signal peptide; variable region.
 SOURCE mouse
 ORGANISM Mus musculus
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and Imanishi-Kari,T.
 TITLE Heavy chain variable region: Multiple gene segments encode anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
 JOURNAL J. Exp. Med. 161, 1272-1292 (1985)
 STANDARD full automatic
 COMMENT #source: strain=Balb-c;

Serological analysis of hybridoma proteins resulting from the immune response to the hapten NP reveals NP(a) idiotypes expressed by Balb/C mice and NP(b) idiotypes expressed by C57 BL/6 mice. The NP(b) family of antibodies consists of 6 subgroups (I-VI) with I-IV sharing more determinants than V and VI which appear quite distinct.

FEATURES Location/Qualifiers
 sig_peptide 1..57
 misc_feature 58..351
 /note="variable region (aa 1-98)"
 misc_feature 148..162
 /note="CDR 1"
 misc_feature 205..255
 /note="CDR 2"
 misc_feature 352..366
 /note="D-region (aa 99-103)"
 misc_feature 367..>414
 /note="J-region (aa 104-119)"
 CDS join(58..351,352..366,367..414)
 /product="idiotypic anti-NP IgG(1) heavy chain V-J"
 /codon_start=1
 /translation="EVQLQQSGAELVRPGASVKLSCTASGFNIKDTYMHVVKQRPEQG
 LEWIGRIDPANGNTKYDPKFGKATITADTSSNTAYLQLSSLTSEDYVYYCASRYE
 RAWFAYWGQGTLLVTVSA"
 BASE COUNT 101 a 98 c 118 g 97 t
 ORIGIN

Initial Score = 281 Optimized Score = 314 Significance = 18.81
 Residue Identity = 88% Matches = 321 Mismatches = 31
 Gaps = 10 Conservative Substitutions = 0

```

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                                GTCAAACTGCAGCAGTCTGGGG
                                || | |||||
GCTGGGTATGTTCTTCTCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTAGCTGCAGCAGTCTGGGG
    20      30      40      50      60      70      80

    30      40      50      60      70      80      90
CAGAGCTTGTAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
|||||
CAGAGCTTGTAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
    90      100     110     120     130     140     150

    100     110     120     130     140     150     160
ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
|||||
ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
    160     170     180     190     200     210     220

    170     180     190     200     210     220     230
  
```


ATACTAAATATGACCCGAAGTTCAGGGCAAGGCCACTATAACAGCAGACACATCTCCAACACAGCCTACC
 |||||
 230 240 250 260 270 280 290
 240 250 260 270 280 290 300
 TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGC-AGACGGAATGTGGGTATCAACG
 |||||
 TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTAG-----TTATAGGTA-CGAGA
 300 310 320 330 340 350 360
 310 320 330 340 350 360
 GGATATGCTCTGGACTT-CTGGGGCCAAGGGACACGGTCACCGTCTCCTCA
 || || || || |||||
 GGGCCTGGTTTG--CTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
 370 380 390 400 410 X

6. US-07-977-702-1 (1-360)

MMV20292B M.musculus mRNA for VH-gen sequence of naturally o

LOCUS MMV20292B 363 bp RNA ROD 23-JUN-1992
 DEFINITION M.musculus mRNA for VH-gen sequence of naturally occurring,
 somatically mutated memory B cell
 ACCESSION Z12783 X59730
 KEYWORDS somatic mutation.
 SOURCE mouse
 ORGANISM Mus musculus
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 363)
 AUTHORS Schitteck, B. and Rajewsky, K.
 TITLE Natural occurrence and origin of somatically mutated memory B cells
 in mice
 JOURNAL J. Exp. Med. 0, 0-0 (1992)
 STANDARD full automatic
 REFERENCE 2 (bases 1 to 363)
 AUTHORS Schitteck, B.
 TITLE Direct Submission
 JOURNAL Submitted (07-JUN-1992) B. Schitteck, Institut of Genetics, Weyertal
 121, W-5000 Cologne, FRG
 STANDARD full automatic
 COMMENT #source: strain=C57BL/6;
 #source: haplotype=IgHb;
 #source: stage=Adult;
 #source: tissue=Spleen;
 #source: cell_type=B-cell;
 #source: clone_library=cDNA library specifically amplified;
 #source: clone=V2029_2B;
 #source: isolate=V2029_2B;
 #source: sex=Female;
 #source: is_macronuclear=N;
 #source: is_proviral=N;
 #source: is_germline=N.
 BASE COUNT 89 a 91 c 102 g 81 t
 ORIGIN

Initial Score = 276 Optimized Score = 282 Significance = 18.44
 Residue Identity = 78% Matches = 287 Mismatches = 69
 Gaps = 8 Conservative Substitutions = 0

X 10 20 30 40 50 60
 GTCAAAGTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGCTCTGCACAGCT
 ||| |||||
 CAGGTCCAAGTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTCAGTGAAGCTGCTCTGCAAGGCT
 X 10 20 30 40 50 60 70


```

X      10      20
GTCAAAGTGCAGCAGTCTGGGG
|| | |||||
GTGACAGTGGCAATCACTTTGCCCTTTCTTTCTACAGGGGTCAATTGAGAGTTTCTGAGTGCAGCAGTCTGGGG
100      110      120      130      140      X 150      160

30      40      50      60      70      80      90
CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
|||||
CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
170      180      190      200      210      220      230

100      110      120      130      140      150      160
ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
|||||
ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
240      250      260      270      280      290      300      310

170      180      190      200      210      220      230
ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
|||||
ATACTAAATATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
320      330      340      350      360      370      380

240      250      260      270      280      290      300      X
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGG-AATGTGGGTATCAACG
|||||
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGC-TACGGTCCCCTGGTA-CTTC
390      400      410      420      430      440      450 X

310      320      330      340      350
GGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCT

```

8. US-07-977-702-1 (1-360)

MMIGVDJAA M.musculus immunoglobulin heavy chain VDJ complex

ID MMIGVDJAA standard; DNA; ROD: 452 BP.
XX
AC Z21679;
XX
DT 17-FEB-1993 (Rel. 35, Created)
DT 17-FEB-1993 (Rel. 35, Last updated, Version 1)
XX
DE M.musculus immunoglobulin heavy chain VDJ complex gene.
XX
KW immunoglobulin heavy chain; VDJ complex.
XX
OS Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
XX
RN [1]
RP 1-452
RA Shirasawa T., Miyazoe I., Hagiwara S., Kimoto H., Shigemoto K.,
RA Taniguchi M., Takenori T.;
RT "Heavy Chain Variable (VH) Region Diversity Generated by VH Gene
RT Replacement in the Progeny of a Single Precursor Cell Transformed
RT with a Temperature-sensitive Mutant of Abelson Murine Leukemia
RT Virus";
RL J. Exp. Med. 176:1209-1214(1992).
XX
RN [2]
RP 1-452
RA Shirasawa T.;

RL Submitted (27-JAN-1993) on tape to the EMBL Data Library by:
RL Takuji Shirasawa, Molecular Pathology, Tokyo Metropolitan Institute
RL of Gerontology, 35-2 Sakae-cho, Itabashi-ku, Tokyo, 173, Japan

XX
CC #source: strain=BALB/c;
CC #source: cell_line=pre-B cell;
CC #source: clone_library=pre-B cell;
CC #source: clone=VDJ;
CC #source: is_macronuclear=N;
CC #source: is_proviral=N;
CC #source: is_germline=N;

XX
FH Key Location/Qualifiers
FH
FT exon 7..52
FT /number=1
FT intron 53..131
FT exon 132..452
FT /number=2
FT CDS join(7..52,132..>452)
FT /product="VDJ complex"
FT misc_feature 432..439
FT /note="D region"
FT misc_feature 440..442
FT /note="N sequence"
FT misc_feature 443..452
FT /note="J region"

XX
SQ Sequence 452 BP; 113 A; 115 C; 115 G; 109 T; 0 other;

Initial Score = 276 Optimized Score = 281 Significance = 18.44
Residue Identity = 91% Matches = 284 Mismatches = 22
Gaps = 3 Conservative Substitutions = 0

X 10 20
GTCAAAGTGCAGCAGTCTGGGG
|||

GTGACAGTGGCAATCACTTTGCCCTTTCTTTCTACAGGGGTCAATTCAGAGGTTTCAGCTGCAGCAGTCTGGGG
100 110 120 130 140 X 150 160

30 40 50 60 70 80 90
CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
|||||
CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
170 180 190 200 210 220 230

100 110 120 130 140 150 160
ATATGCACTGGGTGAAGCAGAGGCCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
|||||
ATATGCACTGGGTGAAGCAGAGGCCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
240 250 260 270 280 290 300 310

170 180 190 200 210 220 230
ATACTAAATATGACCCGAAGTTCAGGTCAGGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
|||||
ATACTAAATATGACCCGAAGTTCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
320 330 340 350 360 370 380

240 250 260 270 280 290 300 X
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGG-AATGTGGGTATCAACG
|||||
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGC-TACGGTTCCCCTGGTA-CTTC
390 400 410 420 430 440 450 X

310 320 330 340 350

9. US-07-977-702-1 (1-360)

MUSIGHNPG Mouse Ig active H-chain mRNA, V-region (VDJ) from

LOCUS MUSIGHNPG 414 bp ss-mRNA ROD 01-SEP-1988
 DEFINITION Mouse Ig active H-chain mRNA, V-region (VDJ) from anti-NP hybridoma P3.6.5.
 ACCESSION M12750
 KEYWORDS immunoglobulin; immunoglobulin heavy chain; variable region.
 SOURCE Mouse (C57BL/6) group V hybridoma P3.6.5, cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
 Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS Boersch-Supan, M.E., Agarwal, S., White-Scharf, M.E. and
 Imanishi-Kari, T.
 TITLE Heavy chain variable region Multiple gene segments encode
 anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
 JOURNAL J. Exp. Med. 161, 1272-1292 (1985)
 STANDARD full automatic
 FEATURES Location/Qualifiers
 sig_peptide 1..57
 /codon_start=1
 /note="Ig H-chain V-region signal peptide"
 mat_peptide 58..414
 /codon_start=1
 /note="Ig H-chain V-region"
 misc_recomb 351..352
 /note="V-region end/D-region start"
 misc_recomb 372..373
 /note="D-region end/J-region start"
 CDS 1..414
 /note="Ig H-chain; (VDJ-region) precursor"
 /codon_start=1
 /translation="MKCSNIMFFLMAVVTGVNSEVQLQSGAELVRPGASVKLSCTAS
 GFNIKDTYMHVVKQRTQGLEWIGRIDPEDGETKYAPKFQVKATITADTSSNTAYLQL
 SSLTSEDTAVYYCARYYYGSSFFAYWGQGLVTVSA"
 BASE COUNT 103 a 99 c 113 g 99 t
 ORIGIN Chromosome 12.

Initial Score = 273 Optimized Score = 309 Significance = 18.22
 Residue Identity = 87% Matches = 317 Mismatches = 34
 Gaps = 12 Conservative Substitutions = 0

```

                                X      10      20
                                GTCAAACTGCAGCAGTCTGGGG
                                || | |||||
GCTGGATCATGTTCTTCTCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTACGCTGCAGCAGTCTGGGG
    20      30      40      50      60      70      80

    30      40      50      60      70      80      90
CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CAGAGCTTGTGAGGCCAGGGGCCTCAGTCAAGTTGTCTGCACGGCTTCTGGCTTCAACATTAAAGACACCT
    90     100     110     120     130     140     150

    100     110     120     130     140     150     160
ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATATGCACTGGGTGAAGCAGAGGACTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGAGGATGGTG
    160     170     180     190     200     210     220

    170     180     190     200     210     220     230
ATACTAAATATGACCCGAAGTTCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC

```

```

AAACTAAATATGCCCCGAAATTCAGGTCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
230      240      250      260      270      280      290

240      250      260      270      280      290      300
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGC-AGACGGAATGTGGGTATCAACG
|||||
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTAGA---TAT-----TA-CTACG
300      310      320      330      340      350      360

310      320      330      340      350      360
GGA-TATGCTCTGGACTT-CTGGGGCCAAGGGACCACGGTCACCGTCTCTCTCA
| | | | |
GTAGTAGCTTCTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
370      380      390      400      410      X

```

10. US-07-977-702-1 (1-360)

MMIGGNP8 Mouse mRNA for idiotypic anti-NP IgG(1) heavy chain

LOCUS MMIGGNP8 414 bp RNA ROD 07-MAY-1992
 DEFINITION Mouse mRNA for idiotypic anti-NP IgG(1) heavy chain V-D-J
 (hybridoma P.3.6.5)
 ACCESSION X02569 M12750
 KEYWORDS gamma-immunoglobulin; Ig D-segment; Ig heavy chain; immunoglobulin;
 joining region; signal peptide; variable region.
 SOURCE mouse
 ORGANISM Mus musculus
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and
 Imanishi-Kari,T.
 TITLE Heavy chain variable region: Multiple gene segments encode
 anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
 JOURNAL J. Exp. Med. 161, 1272-1292 (1985)
 STANDARD full automatic
 COMMENT *source: strain=C57BL/6;

Serological analysis of hybridonaproteins resulting from the immune response to the hapten NP reveals NP(a) idiotypes expressed by Balb/C mice and NP(b) idiotypes expressed by C57 BL/6 mice. The NP(b) family of antibodies consists of 6 subgroups (I-VI) with I-IV sharing more determinants than V and VI which appear quite distinct.

FEATURES Location/Qualifiers
 sig_peptide 1..57
 mat_peptide join(58..147,352..414)
 /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
 misc_feature 58..147
 /note="V-region (aa 1-98)"
 misc_feature 148..162
 /note="CDR I"
 misc_feature 205..255
 /note="CDR II"
 misc_feature 352..372
 /note="D-region (aa 99-105)"
 misc_feature 373..>414
 /note="J-region (aa 106-119)"
 CDS join(1..147,352..414)
 /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
 /codon_start=1
 /translation="MKCSWIMFFLMAVVTGVNSEVQLQSGAELVRPGASVKWSTAS
 GFNIKYYYGSSFFAYWGGTLTVSA"

BASE COUNT 102 a 100 c 114 g 98 t
 ORIGIN

Initial Score = 273 Optimized Score = 307 Significance = 18.22
 Residue Identity = 86% Matches = 314 Mismatches = 38
 Gaps = 10 Conservative Substitutions = 0

```

                                X      10      20
                                GTCAAACTGCAGCAGTCTGGGG
                                || | ||||| ||||| |||||
GCTGGATCATGTTCTTCTCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTAGCTGCAGCAGTCTGGGG
  20      30      40      50      60      70      80

  30      40      50      60      70      80      90
CAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CAGAGCTTGTGAGGCCAGGGGCTCAGTCAAGTGGTCTGCACGGCTTCTGGCTTCAACATTAAAGACACCT
  90     100     110     120     130     140     150

  100     110     120     130     140     150     160
ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATATGCACTGGGTGAAGCAGAGGCTGAACAGGGCTGGAGTGGATTGGAAGGATTGATCCTGAGGATGGTG
  160     170     180     190     200     210     220

  170     180     190     200     210     220     230
ATACTAAATATGACCCGAAGTTCAGGTCAAGGCCACTATTACAGCGGACACGTCTCCAACACAGCCTGGC
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AAACTAAATATGCCCGAAATTCAGGTCAAGGCCACTATAACAGCAGACACATCTCCAACACAGCCTACC
  230     240     250     260     270     280     290

  240     250     260     270     280     290     300     310
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGGAATGTGGGTATCAACGG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGC--TAGCTAT-----TA-CTACGG
  300     310     320     330     340     350     360

  320     330     340     350     360
GA-TATGCTCTGGACTT-CTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
| || ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TAGTAGCTTCTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
  370     380     390     400     410 X

```

11. US-07-977-702-1 (1-360)

MUSIGHNPB Mouse Ig active H-chain mRNA, V-region (VDJ) from

LOCUS MUSIGHNPB 414 bp ss-mRNA ROD 01-SEP-1988
 DEFINITION Mouse Ig active H-chain mRNA, V-region (VDJ) from anti-NP hybridoma P5.40.1.
 ACCESSION M12745
 KEYWORDS immunoglobulin; immunoglobulin heavy chain; variable region.
 SOURCE Mouse (C57BL/6) group VI hybridoma P5.40.1, cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
 Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS Boersch-Supan, M.E., Agarwal, S., White-Scharf, M.E. and Imanishi-Kari, T.
 TITLE Heavy chain variable region Multiple gene segments encode anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
 JOURNAL J. Exp. Med. 161, 1272-1292 (1985)
 STANDARD full automatic
 FEATURES Location/Qualifiers
 sig_peptide 1..57
 /codon_start=1
 /note="Ig H-chain V-region signal peptide"
 mat_peptide 58..>414

ORGANISM MUS MUSCULUS
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and
 Imanishi-Kari,T.
 TITLE Heavy chain variable region: Multiple gene segments encode
 anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
 JOURNAL J. Exp. Med. 161, 1272-1292 (1985)
 STANDARD full automatic
 COMMENT *source: strain=C57 BL/6;

Serological analysis of hybridonaproteins resulting from the immune
 response to the hapten NP reveals NP(a) idiotypes expressed by
 Balb/C mice and NP(b) idiotypes expressed by C57 BL/6 mice. The
 NP(b) family of antibodies consists of 6 subgroups (I-VI) with I-IV
 sharing more determinants than V and VI which appear quite
 distinct.

FEATURES Location/Qualifiers
 sig_peptide 1..57
 mat_peptide join(58..351,352..371,372..414)
 /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
 misc_feature 58..351
 /note="variable region"
 misc_feature 148..162
 /note="CDR I"
 misc_feature 205..255
 /note="CDR II"
 misc_feature 352..371
 /note="D-region (aa 99-105)"
 misc_feature 372..>414
 /note="J-region (aa 106-119)"
 CDS join(1..351,352..371,372..414)
 /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
 /codon_start=1
 /translation="MKFSWVMFFLMAVVTGVNSEVQLQSSVAELVRPGASVKLSCTAS
 GFNIKNTYMHVVKQRPEQGLEWIGRIDPANGSTKYAPKFQIKATITADTSSNTAYLQL
 SSLTSEDTAIYYCARYYYESSLFAYWGQGT LVTVSA"

BASE COUNT 102 a 101 c 111 g 100 t
 ORIGIN

Initial Score = 272 Optimized Score = 308 Significance = 18.14
 Residue Identity = 87% Matches = 315 Mismatches = 37
 Gaps = 10 Conservative Substitutions = 0

```

                                X      10      20
                                GTCAAACTGCAGCAGTCTGGGG
                                || | ||||| ||||| ||
GCTGGGTCATGTTCTTCTCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTACGCTGCAGCAGTCTGTGG
      20      30      40      50      60      70      80

      30      40      50      60      70      80      90
CAGAGCTTGTAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CAGAGCTTGTAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAAACACCT
      90     100     110     120     130     140     150

     100     110     120     130     140     150     160
ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
     160     170     180     190     200     210     220

     170     180     190     200     210     220     230
ATACTAAATATGACCCGAAGTTCAGGTCAAGGCCACTATTACAGGGGACACGTCCTCCAACACAGCCTGGC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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GTACTAAGTATGCCCGAAGTTCAGATCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
 230 240 250 260 270 280 290
 240 250 260 270 280 290 300 310
 TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGGAATGTGGGTATCAACGG
 |||||
 TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCATCTATTACTGTGC--TAGGTAT-----TA-CTACGA
 300 310 320 330 340 350 360
 320 330 340 350 360
 GA-TATGCTCTGGACTT-CTGGGGCCAAGGACACGGTCACCGTCTCCTCA
 || || || || |||||
 GAGTAGCCTGTTTGCTTACTGGGGCCAAGGACTCTGGTCACTGTCTCTGCA
 370 380 390 400 410 X

13. US-07-977-702-1 (1-360)

MMIGG1HCV M.musculus rearranged mRNA for anti-cytochrome c i

LOCUS MMIGG1HCV 351 bp RNA ROD 21-NOV-1991
 DEFINITION M.musculus rearranged mRNA for anti-cytochrome c immunoglobulin G1
 (IgG1) heavy chain variable region
 ACCESSION X60683
 KEYWORDS Anti-cytochrome c immunoglobulin G1; E8 variable heavy chain;
 E8 variable heavy chain D region; E8 variable heavy chain J region;
 E8 variable heavy chain V region; IgG1.
 SOURCE mouse
 ORGANISM Mus musculus
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 351)
 AUTHORS Mylvaganam,S.E.
 TITLE Direct Submission
 JOURNAL Submitted (05-JUL-1991) S.E. Mylvaganam, Dept of Mol Biology, MB4,
 The Scripps Research Inst 10666 N. Torrey Pines Rd, La Jolla, CA
 92037, USA
 STANDARD full automatic
 REFERENCE 2 (bases 1 to 351)
 AUTHORS Mylvaganam,S.E., Paterson,Y., Kaiser,K., Bowdish,K. and
 Getzoff,E.D.
 TITLE Biochemical Implications from the Variable Gene Sequences of an
 Anti-cytochrome c Antibody and Crystallographic Characterization of
 its Antigen-binding Fragment in Free and Antigen-complexed Forms
 JOURNAL J. Mol. Biol. 221, 455-462 (1991)
 STANDARD full automatic
 COMMENT *source: strain=BAKB/c;
 *source: cell_type=myeloma;
 *source: cell_line=CA4-1;

E8 is a monoclonal antibody of the anti-cytochrome c immunoglobulin
 G1 (IgG1) that binds horse cytochrome c. E8 variable light chain -
 X60684

E8 variable heavy chain - X60683.

FEATURES Location/Qualifiers
 misc_feature 1..282
 /note="heavy variable region"
 misc_feature 91..105
 /note="first hyper-variable region"
 misc_feature 148..198
 /note="second hyper-variable region"
 misc_feature 295..318
 /note="third hyper-variable region"
 misc_feature 283..315
 /note="D region"
 misc_feature 316..352
 /note="J region"

<1.7>351
 /product="E8 variable heavy chain"
 /codon_start=1
 /translation="EVQLQQSGAELVKPGASVKLSCTASGFNIDTYMHNVKQRPEKG
 LEWIGRIDPASGNTKYDPKFQDKATITADTSSNTAYLQLSSLTSEDYAVYYCAGYDYG
 NFDYWGGGTTTLTVSS"

BASE COUNT 92 a 92 c 91 g 76 t
 ORIGIN

Initial Score = 271 Optimized Score = 316 Significance = 18.07
 Residue Identity = 89% Matches = 323 Mismatches = 25
 Gaps = 12 Conservative Substitutions = 0

```

      X      10      20      30      40      50      60
      GTCAAAGTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCT
      || | |||||
      GAGGTTGAGTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCCTGCACAGCT
      X      10      20      30      40      50      60      70

70      80      90      100     110     120     130     140
      TCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATT
      |||||
      TCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAAAAGGGCCTGGAGTGGATT
      80      90      100     110     120     130     140

      150     160     170     180     190     200     210
      GGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCAGGTCAAGGCCACTATTACAGCG
      |||||
      GGAAGGATTGATCCTGCGAGTGGTAATACTAAATATGACCCGAAGTTCAGGACAAGGCCACTATAACAGCA
      150     160     170     180     190     200     210

      220     230     240     250     260     270     280
      GACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGT
      |||||
      GACACATCCTCCAACACAGCCTACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGT
      220     230     240     250     260     270     280

      290     300     310     320     330     340     350
      GCAGACGGAATGTGGGTATCAACGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCC
      || | | ||| || |||| | || | ||||| ||||| ||||| |||||
      GCTG--GTTATG-----AT-TACGGCA---ACTTT-GACTACTGGGGCCAAGGCACCACTCTCACAGTCTCC
      290           300           310           320           330           340

```

X
 TCA
 |||
 TCA
 350

14. US-07-977-702-1 (1-360)

MUSIGMU4G Mouse monoclonal antiidiotypic antibody IgM VDJ-re

LOCUS MUSIGMU4G 354 bp ss-mRNA ROD 16-JUL-1992
 DEFINITION Mouse monoclonal antiidiotypic antibody IgM VDJ-region mRNA.
 ACCESSION M83722
 KEYWORDS diversity region; immunoglobulin heavy chain;
 immunoglobulin mu-chain; joining region;
 monoclonal antiidiotypic antibody; variable region.
 SOURCE Mus musculus hybridoma cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
 Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 354)
 AUTHORS Taub,R., Hsu,J.-C., Garsky,V.M., Hill,B.L., Erlanger,B.F. and
 Kohn,L.D.

LOCUS	MUSIGHBB	390 bp ss-mRNA	RDD	30-JUN-1987
DEFINITION	Mouse Ig active mu-chain VDJ-region mRNA from hybridoma 87.92.6.			
ACCESSION	M13832			
KEYWORDS	constant region; diversity region; immunoglobulin heavy chain;			

IMMUNOGLOBULIN MU-CHAIN; joining region; processed gene;
variable region.

SOURCE Mouse (Balb/c) hybridoma 87.92.6 (mu,kappa), cDNA to mRNA.

ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 390)

AUTHORS Bruck,C., Co,M.S., Slaoui,M., Gaulton,G.N., Smith,T., Fields,B.N.,
Mullins,J.I. and Greene,M.I.

TITLE Nucleic acid sequence of an internal image-bearing monoclonal
anti-idiotypic and its comparison to the sequence of the external
antigen

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83, 6578-6582 (1986)

STANDARD full automatic

FEATURES Location/Qualifiers

sig_peptide <1..30
/codon_start=1
/note="Immunoglobulin mu-chain signal peptide"

mat_peptide 31..390
/codon_start=1
/note="Immunoglobulin mu-chain"

misc_recomb 327..328
/note="V-region end/D-region start"

misc_recomb 342..343
/note="D-region end/J-region start"

CDS <1..390
/note="Immunoglobulin mu-chain precursor"
/codon_start=1
/translation="LMAVVTGVNSEVQLQSGAELVKPGASVKLSCTASGFNIDTYM
HWVKQRPEQGLEWIGRIDPANGNTKYDPKFQKGATITADTSSNTAYLQLSSLTSEDTA
VYYCARGGLRRGYAMDYWGQGTSVTVSS"

BASE COUNT 100 a 96 c 111 g 83 t

ORIGIN 44 bp upstream of PstI site; chromosome 12.

Initial Score = 271 Optimized Score = 326 Significance = 18.07
Residue Identity = 91% Matches = 330 Mismatches = 25
Gaps = 7 Conservative Substitutions = 0

```

                                X      10      20      30
                                GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCA
                                || | ||||| ||||| ||||| ||||| ||||| |||||
CTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTAGCTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCA
      10      20      30 X      40      50      60      70

40      50      60      70      80      90      100     110
GGGGCCTCAGTCAAGTTGTCTGCACAGCTTCTGGCTTCAACATTAAGACACCTATATGCACTGGGTGAAG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GGGGCCTCAGTCAAGTTGTCTGCACAGCTTCTGGCTTCAACATTAAGACACCTATATGCACTGGGTGAAG
      80      90      100     110     120     130     140

      120     130     140     150     160     170     180
CAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTAATACTAAATATGACCCG
      150     160     170     180     190     200     210

      190     200     210     220     230     240     250
AAGTTCCAGGTCAAGGCCACTATTACAGCGGACAGCTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACCTGCAGCTCAGCAGCCTG
      220     230     240     250     260     270     280

      260     270     280     290     300     310     320
ACATCTGAGGACACTGCCGTCTACTACTGTGC-AGACGGAATGTGGGTATCAAC-GGGATATGCTCTGGACT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ACATCTGAGGACACTGCCGTCTATTACTGTGCTAGAGGG-----GGATTACGACGGGGGTATGCTATGGACT

```

```

290      300      310      320      330      340      350
330      340      350      X
TCTGGGGCCAAGGGACCGGTCACCGTCTCCTCA
||||| ||||| ||| | ||||| |||||
ACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
360      370      380      390

```

Seq. 2

```

> 0 <
0| 0 IntelliGenetics
> 0 <

```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

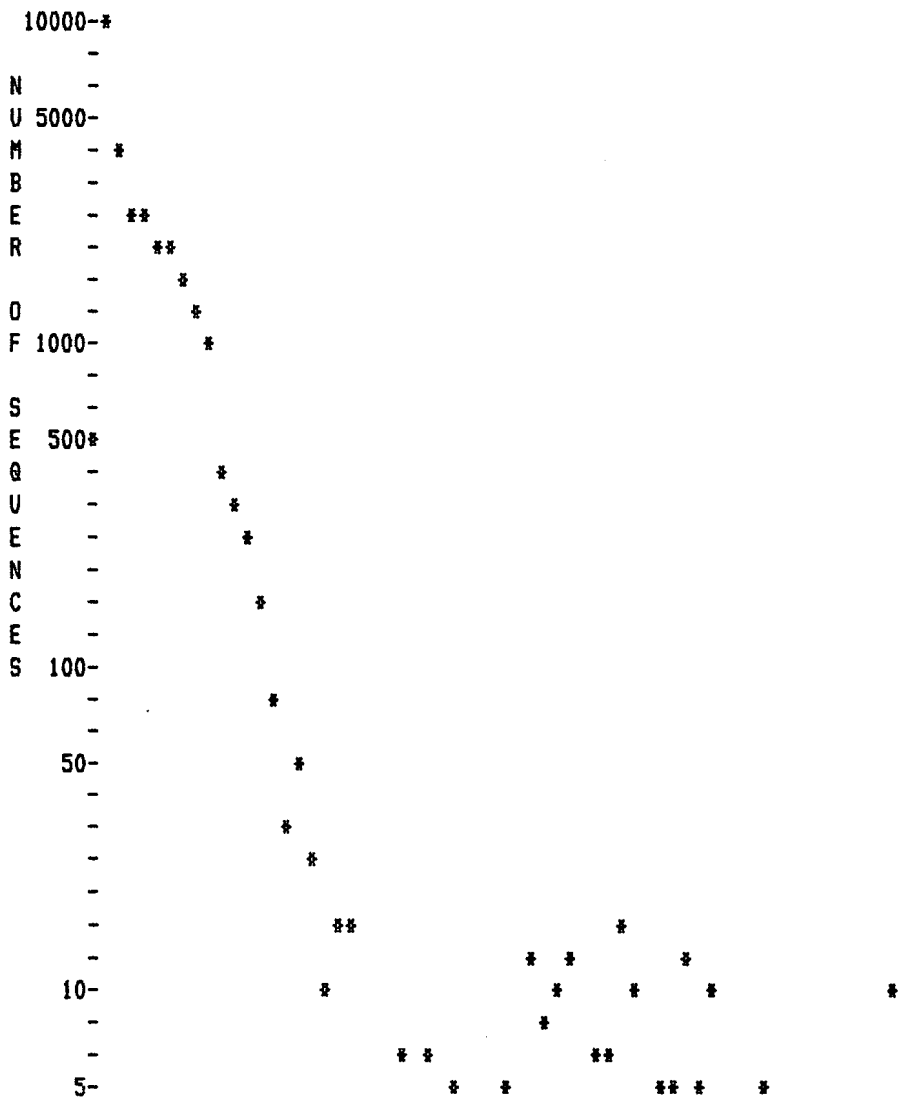
Results file us-07-977-702-2-ngs.res made by shears on Tue 15 Jun 93 11:11:14-PDT.

```

Query sequence being compared:US-07-977-702-2 (1-318)
Number of sequences searched:      25646
Number of scores above cutoff:    4637

```

Results of the initial comparison of US-07-977-702-2 (1-318) with:
Data bank : N-GeneSeq 10, all entries



```

-      *      *      *      *      *      *
-
-
-
-
0-----
| | | | | | | | | | | | | | | |
SCORE 0 | 29 | 58 | 88 | 117 | 146 | 175 | 205 | 234 | 263
STDEV  0  1  2  3  4  5  6  7  8  9

```

PARAMETERS

```

Similarity matrix      Unitary      K-tuple      4
Mismatch penalty      1      Joining penalty      30
Gap penalty      1.00      Window size      32
Gap size penalty      0.33
Cutoff score      0
Randomization group      0

```

```

Initial scores to save      40      Alignments to save      15
Optimized scores to save      0      Display context      50

```

SEARCH STATISTICS

```

Scores:      Mean      Median      Standard Deviation
              17      14      12.85

```

```

Times:      CPU      Total Elapsed
              00:03:01.00      00:06:12.00

```

```

Number of residues:      14371384
Number of sequences searched:      25646
Number of scores above cutoff:      4637

```

```

Cut-off raised to 8.
Cut-off raised to 15.
Cut-off raised to 22.
Cut-off raised to 26.
Cut-off raised to 29.

```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
**** 19 standard deviations above mean ****						
1. Q04265	Encodes Colon Cancer monoclon	381	263	265	19.14	0
**** 18 standard deviations above mean ****						
2. Q28254	VL FRP5.	407	260	263	18.91	0
3. Q28653	DNA encoding 1E6 kappa light	327	257	260	18.68	0
4. Q28262	Fv(FRP5)-ETA fusion gene.	2011	257	260	18.68	0
5. Q28257	Fv(FRP5)-phoA recombinant ant	2233	257	260	18.68	0
6. Q04592	Sequence encoding region of h	324	256	257	18.60	0
7. N90813	DNA encoding light chain vari	324	256	257	18.60	0
8. Q27132	Light chain variable region c	387	256	257	18.60	0
9. Q28256	Fv heavy chain/light chain va	748	256	259	18.60	0
10. Q05557	Sequence encoding variable re	411	255	259	18.52	0
11. N40022	cDNA insert of pK17G4 encodin	882	252	254	18.29	0
12. Q04264	Encodes Colon Cancer monoclon	685	250	253	18.13	0

13. N40023	MMNA encoding kappa anti-Carc	882	249	253	18.06	0
**** 16 standard deviations above mean ****						
14. Q25592	Encodes 4D5 Fab IgG antibody	2178	234	237	16.89	0
15. Q28747	Anti-CEA specific light chain	387	227	257	16.34	0
**** 15 standard deviations above mean ****						
16. N81636	Anti-pseudomonas aeruginosa h	324	216	219	15.49	0
17. N81638	Anti-pseudomonas aeruginosa h	671	216	220	15.49	0
18. Q10946	Feline immunoglobulin kappa c	618	214	221	15.33	0
19. Q11191	V region gene JP2gL411 from a	618	214	221	15.33	0
20. Q04654	Plasmid pBT111 encoding antib	5238	213	214	15.25	0
21. Q29150	WN1 222-5 antibody Light chai	322	210	215	15.02	0
**** 14 standard deviations above mean ****						
22. Q12017	Sequence encoding mouse MAb 1	402	208	216	14.86	0
23. Q12061	Sequence encoding light (kapp	402	208	216	14.86	0
24. Q29151	WN1 58-9 antibody Light chain	321	204	213	14.55	0
25. Q15114	IL-2 chimeric antibody light	432	204	211	14.55	0
26. Q23566	Rat CD4 antibody light chain	620	204	209	14.55	0
27. Q05556	Sequence encoding variable re	419	200	210	14.24	0
28. N90672	DNA sequence encoding uproces	420	200	208	14.24	0
29. Q15113	IL-2 chimeric antibody light	432	200	207	14.24	0
30. Q08608	ME4 Light Chain V Region (mou	444	200	208	14.24	0
31. Q12633	CD4-specific CDR-grafted ligh	754	200	208	14.24	0
32. N90500	Light chain antibody variable	608	198	206	14.09	0
33. Q23567	Reshaped CAMPATH-1 antibody l	748	198	206	14.09	0
34. Q20381	Sequence encoding the shorten	819	198	208	14.09	0
35. Q23568	Reshaped CD4 antibody light c	748	197	205	14.01	0
36. N90300	Insert coding for light chain	1395	197	207	14.01	0
**** 13 standard deviations above mean ****						
37. Q11848	Human anti-placental alkaline	324	194	204	13.77	0
38. Q21097	FabD1.3 in pUC19.	1526	194	203	13.77	0
39. Q11846	Anti-placental alkaline phosp	324	193	203	13.70	0
40. N30165	Sequence encoding the leader,	450	192	199	13.62	0

1. US-07-977-702-2 (1-318)

Q04265 Encodes Colon Cancer monoclonal antibody CC92 ligh

ID Q04265 standard; DNA; 381 BP.
AC Q04265;
DT 13-SEP-1990 (first entry)
DE Encodes Colon Cancer monoclonal antibody CC92 light chain variable region
KW chimeric antibodies; TAG72; light chain variable region;
KW heavy chain variable region; ss
OS synthetic.
PN EP-365997-A.
PD 02-MAY-1990.
PF 18-OCT-1989; 119361.
PR 19-OCT-1988;US-259943.
PA (DOWC) Dow Chemical Co.
PI Mezes P, Gourlie B, Rixon M;
DR WPI; 90-133521/18.
DR P-PSDB; R04388.
PT Chimeric antibodies against TAG72 and conjugate to provide imaging
PT markers and therapeutic tools
PS Disclosure; pp; English.
CC The polypeptide encoded by this sequence forms part of a chimera. The
CC other components are a heavy chain variable region and human-derived
CC constant light and heavy chain regions. The variable regions have
CC high affinity for TAG72. The constant regions reduce the side-effects
CC when administered to human patients because they are of human origin.
CC See also Q04258-64 and Q04266-9.
SQ Sequence 381 BP; 90 A; 90 C; 97 G; 104 T;

Initial Score = 263 Optimized Score = 265 Significance = 19.14
Residue Identity = 83% Matches = 266 Mismatches = 52
Gaps = 1 Conservative Substitutions = 0


```

X      10      20
AG-TATTGTGATGACCCAGACT
|| |||||
AGATCCAGGTCCTTTGTATTCTGTTCTCTGGTGTCTGGTGTGACGGAGACATTGTGATGACCCAGTCT
10      20      30      40      50      60      70

30      40      50      60      70      80      90
CCCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAAT
| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CACAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGAGTAGT
80      90      100      110      120      130      140      150

100      110      120      130      140      150      160
GATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTAC
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GCTGTAGGGTGGTTTCAACAGAAACCAGGACAATCTCCTAAATTACTGATTTATTCGGCATCCTACCGGTAT
160      170      180      190      200      210      220

170      180      190      200      210      220      230
ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTACCATCAGCACTGTGCAG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTCGGACGGATTTCACTTTACCATCACCAGTGTGCAG
230      240      250      260      270      280      290

240      250      260      270      280      290      300
GCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCCGAGGGGGGACCAAG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GCTGAAGACCTGGCAGTTTATTACTGTCAGCAACATTATAGTAGTCCGCTCACGTTCCGGTCTGGGACCAAG
300      310      320      330      340      350      360

310      X
CTGGAGATC
||||| |
CTGGAGCTGAAACT
370      X 380

```

2. US-07-977-702-2 (1-318)

Q28254 VL FRP5.

ID Q28254 standard; DNA; 407 BP.
AC Q28254;
DT 11-FEB-1993 (first entry)
DE VL FRP5.
KW Minigene; pMZ18/1; monoclonal antibody; kappa; light chain;
KW variable region; pMW31; ss.
OS Mus musculus.
PN EP-502812-A.
PD 09-SEP-1992.
PF 27-JAN-1992; 810056.
PR 05-FEB-1991; EP-810079.
PA (CIBA) CIBA GEIGY AG.
PI Groner B, Hardman N, Harwerth I, Hynes NE, Wels WS;
PI Zwickl M;
DR MPI; 92-302096/37.
PT Recombinant antibodies directed to growth factor receptor C-erbB-2 -
PT for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
PT or ovarian tumours
PS Disclosure; Page 29; 67pp; English.
CC The sequence given a portion of the plasmid pMZ18/1 and encodes the
CC kappa light chain variable (V) domain of the monoclonal antibody FRP5.
CC The V-region was excised from this plasmid and cloned into plasmid
CC pMW31 which was used in the construction of a recombinant antibody
CC which is directed to the extracellular domain of the growth factor
CC c-erbB-2.

Sequence 407 BP; 101 A; 107 C; 94 G; 105 T;

Initial Score = 260 Optimized Score = 263 Significance = 18.91
Residue Identity = 82% Matches = 264 Mismatches = 54
Gaps = 1 Conservative Substitutions = 0

```

          X      10      20      30      40
          AG-TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTCAGC
          || ||||| ||||| ||||| ||||| |||||
TCTAGTCACTGGATGGTGGGAAGATGGAGACATTGTGATGACCCAGTCTCACAATTCCTGTCCACTTCAGT
      10      20      30      40      50      60      70

      50      60      70      80      90      100     110
AGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGTATAATGCTGTTGCCTGGTATCAACAGAA
      80      90      100     110     120     130     140

      120     130     140     150     160     170     180
GCCAGGGCAGTCTCTAAACTGCTGATATATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCAC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ACCAGGACAATCTCTAAACTTCTGATTTACTCGGCATCCTCCCGGTACACTGGAGTCCCTTCTCGCTTCAC
      150     160     170     180     190     200     210

      190     200     210     220     230     240     250     260
TGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TGGCAGTGGCTCTGGGCCGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATT
      220     230     240     250     260     270     280

          270     280     290     300     310     X
CTGTCAAGCAGGATTATAGCTCTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAGATC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTGTCAAGCAACATTTTCGTACTCCATTACGTTCCGGCTCGGGGACAAAATTGGAATAAACGGGCTGATGC
      290     300     310     320     330     340     X 350     360

TGCACCAACTGTATCCATCTTCCACCATCCAGTGA
      370     380     390

```

3. US-07-977-702-2 (1-318)

Q28653 DNA encoding 1E6 kappa light chain variable region

ID Q28653 standard; DNA; 327 BP.
AC Q28653;
DT 17-FEB-1993 (first entry)
DE DNA encoding 1E6 kappa light chain variable region.
KW Chimeric; heavy chain; variable region; monoclonal antibody;
KW lymphocyte function associated antigen-3; LFA-3; inflammation;
KW autoimmune disease; immunomodulation; systemic lupus erythematosus;
KW rheumatoid arthritis; thyroiditis; ss.
OS Homo sapiens.
PN EP-503646-A.
PD 16-SEP-1992.
PF 12-MAR-1992; 104318.
PR 12-MAR-1991; US-667975.
PA (BIOJ) BIOGEN INC.
PI Chisholm PL, Sato VL, Wallner BP;
DR WPI; 92-309758/38.
DR P-PSDB; R27144.
PT Monoclonal antibodies active against lymphocyte function
PT associated antigen-3 - for treating inflammation and auto:immune
PT diseases, and for detecting LFA-3 protein in a sample
PS Claim 16; Page 14; 30pp; English.
CC DNA sequences obt'd. from the hybridoma cell line 1E6-2C12 (ATCC HB
CC 10693) encoding the light and heavy chain regions of 1E6 were

CC amplified for cloning and sequencing using PCR. The PCR primers for
 CC the light chain variable region were MKVP7 and 360-41, and the heavy
 CC chain primers were VH01 and VH02. The PCR prods. were
 CC electrophoresed on agarose gel and the DNA excised and inserted into
 CC plasmids. The light and heavy chain regions may be used to
 CC construct a monoclonal antibody active against LFA-3 which blocks
 CC adhesion of LFA-3 expressing cells to lymphocytes. The antibody may
 CC be used in the treatment and diagnosis of acute and chronic
 CC inflammation, autoimmune diseases and for immunomodulation including
 CC systemic lupus erythematosus, rheumatoid arthritis and thyroiditis.
 CC See also Q28654-8.

SQ Sequence 327 BP; 89 A; 82 C; 83 G; 73 T;

Initial Score = 257 Optimized Score = 260 Significance = 18.68
 Residue Identity = 81% Matches = 260 Mismatches = 58
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
|  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AACATTGTAATGACCCAATCTCCCAAATCCATGTCCATGTCTAGTAGAGAGAGGGTCACCTTGACCTGCAAG
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
||||| ||| |||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GCCAGTGAGAAATGTGGTTACTTATGTTTCTGGTATCAACAGAAACCAGAGCAGTCTCCTAAACTGCTCATA
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
||  ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TACGGGGCATCCAACCGGTACACTGGGGTCCCCGATCGCTTACAGGCAGTGGATCTGCAACAGATTTCAC
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTGACAGGATTATAGCTCTCCGTAC
|  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGACAGATTATCACTGTGGACAGGGTTACAGCTATCCGTAC
     220     230     240     250     260     270     280

    290     300     310     X
ACGTTCGGAGGGGGGACCAAGCTGGAGATC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ACGTTCGGAGGGGGGACCAAGCTGGAATAAAACGGGCT
    290     300     310     320

```

4. US-07-977-702-2 (1-318)

Q28262 Fv(FRP5)-ETA fusion gene.

ID Q28262 standard; DNA; 2011 BP.
 AC Q28262;
 DT 11-FEB-1993 (first entry)
 DE Fv(FRP5)-ETA fusion gene.
 KW Monoclonal antibody; light chain; heavy chain; tumour; c-erbB-2;
 KW variable region; ETA; ss.
 OS Pseudomonas aeruginosa PAK.
 FH Key Location/Qualifiers
 FT sig_peptide 1..63
 FT /*tag= a
 FT /label= ompA_signal_peptide
 FT misc_RNA 64..87
 FT /*tag= b
 FT /note= "FLAG peptide and enterokinase cleavage site"
 FT misc_RNA 97..453

FT /*tag= c
 FT /label= FRP5_heavy_chain_variable_domain
 FT misc_RNA 454..498
 FT /*tag= a
 FT /label= Linker
 FT misc_RNA 499..822
 FT /*tag= a
 FT /label= FRP5_light_chain_variable_domain
 FT CDS 826..1911
 FT /*tag= a
 FT /label= ETA_1574-1747
 FT 3'clip 1912..2012
 FT /*tag= a
 FT /label= ETA_3'_non-coding_region
 PN EP-502812-A.
 PD 09-SEP-1992.
 PF 27-JAN-1992; 810056.
 PR 05-FEB-1991; EP-810079.
 PA (CIBA) CIBA GEIGY AG.
 PI Groner B, Hardman N, Harwerth I, Hynes NE, Wells WS;
 PI Zwickl M;
 DR WPI: 92-302096/37.
 DR P-PSDB; R26982.
 PT Recombinant antibodies directed to growth factor receptor C-erbB-2 -
 PT for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
 PT or ovarian tumours
 PS Disclosure; Page 47-52; 67pp; English.
 CC The sequences given in 028261-3 encode part of the exotoxin A (ETA)
 CC sequence corresponding to positions 1574-1747 of the full exotoxin A
 CC sequence. These sequences were used in the construction of
 CC Fv(FRP5)-ETA fusion genes. The ETA sequence was used as a marker gene
 CC so that E. coli transformed with the fusion gene could be identified.
 CC The fusion genes were expressed in E. coli and the antibody was
 CC extracted. This recombinant antibody can be used for the qualitative
 CC and quantitative determination of c-erbB-2. This can be used for
 CC monitoring or in-vivo localisation of tumours overexpressing c-erbB-2.
 SQ Sequence 2011 BP; 383 A; 653 C; 620 G; 355 T;

Initial Score = 257 Optimized Score = 260 Significance = 18.68
 Residue Identity = 81% Matches = 260 Mismatches = 58
 Gaps = 0 Conservative Substitutions = 0

```

                                X      10      20
                                AGTATTGTGATGACCCAGACTC
                                || | ||||| |||
CCTCTGGCGGTGGCGGTTCTGGTGGCGGTGGCTCCGGCGGTGGCGGTTCTGACATCCAGCTGACCCAGTCTC
450      460      470      480      490      500      510      520

      30      40      50      60      70      80      90
CCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ACAAATTCCTGTCCACTTCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGTATAATG
      530      540      550      560      570      580      590

      100      110      120      130      140      150      160
ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
||| || ||||| ||||| ||||| || ||||| ||||| ||||| || ||||| || |||||
CTGTTGCCTGGTATCAACAGAAACCAGGACAATCTCCTAAACTTCTGATTTACTCGGCATCCTCCCGGTACA
      600      610      620      630      640      650      660

      170      180      190      200      210      220      230
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTGGAGTCCCTTCTCGCTTCACTGGCAGTGGCTCTGGGCCGGATTTCACTTTCACCATCAGCACTGTGCAGG
      670      680      690      700      710      720      730
  
```

240 250 260 270 280 290 300 310
 CTGAAGACCTGGCAGTTTATTTCTGTGTCAGCAGGATTATAGCTCTCCGTACACGTTCCGAGGGGGGACCAAGC
 |||||
 CTGAAGACCTGGCAGTTTATTTCTGTGTCAGCAACATTTTCGTA CTCCATTACGTTCCGGCTCGGGGACAAAAT
 740 750 760 770 780 790 800

X
 TGGAGATC
 |||||
 TGGAGATCAAAGCTCTAGAGGGCGGCAGCCTGGCCGCGCTGACCGCGCACCAGGCCTG
 810 X 820 830 840 850 860

5. US-07-977-702-2 (1-318)

Q28257 Fv(FRP5)-phoA recombinant antibody.

ID Q28257 standard; DNA; 2233 BP.
 AC Q28257;
 DT 11-FEB-1993 (first entry)
 DE Fv(FRP5)-phoA recombinant antibody.
 KW Monoclonal antibody; light chain; heavy chain; tumour; phoA;
 KW variable region; alkaline phosphatase; c-erbB-2; ss
 OS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 23..2158
 FT /*tag= a
 FT sig_peptide 23..85
 FT /*tag= b
 FT /label= ompA_signal_peptide
 FT misc_RNA 89..445
 FT /*tag= c
 FT /label= FRP5_heavy_chain_variable_domain
 FT misc_RNA 446..490
 FT /*tag= d
 FT /label= Linker
 FT misc_RNA 491..814
 FT /*tag= e
 FT /label= FRP5_light_chain_variable_domain
 FT mat_peptide 815..2155
 FT /*tag= f
 FT /label= phoA_coding_region
 PN EP-502812-A.
 PD 09-SEP-1992.
 PF 27-JAN-1992; 810056.
 PR 05-FEB-1991; EP-810079.
 PA (CIBA) CIBA GEIGY AG.
 PI Groner B, Hardman N, Harwerth I, Hynes NE, Wels WS;
 PI Zwickl M;
 DR WPI; 92-302096/37.
 DR P-PSDB; R26980.
 PT Recombinant antibodies directed to growth factor receptor C-erbB-2 -
 PT for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
 PT or ovarian tumours
 PS Disclosure; Page 34-40; 67pp; English.
 CC The sequence given encodes the single chain recombinant antibody
 CC desiganted Fv(FRP5)-phoA. The alkaline phosphatase gene (phoA) was
 CC used as a marker gene so that E. coli transformed with the fusion gene
 CC could be identified. The fusion gene was expressed in E. coli and the
 CC antibody was extracted. This recombinant antibody can be used for the
 CC qualitative and quantitative determination of c-erbB-2. This can be
 CC used for monitoring or in-vivo localisation of tumours overexpressing
 CC c-erbB-2.
 SQ Sequence 2233 BP; 566 A; 573 C; 606 G; 488 T;

Initial Score = 257 Optimized Score = 260 Significance = 18.68
 Residue Identity = 81% Matches = 260 Mismatches = 58

Gaps = 0 Conservative Substitutions = 0

```

                                X      10      20
                                AGTATTGTGATGACCCAGACTC
                                ||  | ||||| |||
CCTCTGGCGGTGGCGGTTCTGGTGGCGGTGGCTCCGGCGGTGGCGGTTCTGACATCCAGCTGACCCAGTCTC
  450      460      470      480      490      500      510

  30      40      50      60      70      80      90
CCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
||||||| |||| ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
ACAAATTCCTGCTCACTTCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGTATAATG
  520      530      540      550      560      570      580

 100      110      120      130      140      150      160
ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
||| || ||||| ||||| ||||| || ||||| ||||| ||| ||||| || |||||
CTGTTGCCTGGTATCAACAGAAACCAGGACAATCTCCTAAACTTCTGATTTACTCGGCATCCTCCCGGTACA
  590      600      610      620      630      640      650

 170      180      190      200      210      220      230
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTGGAGTCCCTTCTCGCTTCACTGGCAGTGGCTCTGGGCCGGATTTCACTTTCACCATCAGCAGTGTGCAGG
  660      670      680      690      700      710      720

 240      250      260      270      280      290      300      310
CTGAAGACCTGGCAGTTTATTTCTGTCTCAGCAGGATTATAGCTCTCCGTACACGTTCCGAGGGGGACCAAGC
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTGAAGACCTGGCAGTTTATTTCTGTCTCAGCAACATTTCTGACTCCATTACGTTCCGGCTCGGGGACAAAAT
  730      740      750      760      770      780      790      800

      X
TGGAGATC
|||||||
TGGAGATCAAAGCTCTAGAGCCTGTTCTGGAAAACCGGGCTGCTCAGGGCGATATTAC
      810      820      830      840      850

```

6. US-07-977-702-2 (1-318)

004592 Sequence encoding region of human carcinoembryonic

ID 004592 standard; DNA; 324 BP.
AC 004592;
DT 28-SEP-1990 (first entry)
DE Sequence encoding region of human carcinoembryonic light chain
DE antigen (CEA).
KW Carcinoembryonic antigen; CEA; Chelate-specific antigen; CHA;
KW tumor; cancer; serum sickness.
OS Homo sapiens.
PN EP-369566-A.
PD 23-MAY-1990.
PF 8-MAR-1989; 302313.
PR 17-NOV-1988; US-274105; EP-302313.
PA (HYBR-) Hybritech Inc.
PI Johnson MJ, Phelps JL;
DR WPI; 90-157695/21.
DR P-PSDB; R04936.
PT Bifunctional chimeric antibodies -
PT having variable regions which recognise different antigens and
PT metal chelates and human constant regions.
PS Claim 2; Page 24; 40pp; English.
CC Gene encodes portion of CEA light chain antigen, useful in
CC generating chimeric monoclonal antibody binding to CEA at a tumour
CC site and a metal chelate bonded to say a toxin or other drug.
SQ Sequence 324 BP; 85 A; 83 C; 77 G; 79 T;

Initial Score = 256 Optimized Score = 257 Significance = 18.60
 Residue Identity = 80% Matches = 257 Mismatches = 61
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
|||||
GACATTGTGATGACCCAGTCTCAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAG
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
|||||
GCCAGTCAGAAATGTTCTGACTGCTGTTGCCTGGTATCAACAGAAACCAGGGCAGTCTCCTAAAGCACTGATT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCCTACT
|||
TACTTGGCATCCAACCGGTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCCTACT
     150     160     170     180     190     200     210

    220     230     240     250     260     270     280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCTGACAGGATTATAGCTCTCCGTAC
|||||
CTCACCATTACCAATGTGCAATCTGAAGACCTGGCAGATTATTTCTGTCTGCAACATTGGAATTATCCGCTC
    220     230     240     250     260     270     280

290      300      310      X
ACGTTCTGGAGGGGGGACCAAGCTGGAGATC
|||||
ACGTTCTGGTGGGACCAAGCTGGAGCTGAAACGG
290      300      310      320

```

7. US-07-977-702-2 (1-318)

N90813 DNA encoding light chain variable region against c

ID N90813 standard; cDNA; 324 BP.
 AC N90813;
 DT 24-JAN-1990. (first entry)
 DE DNA encoding light chain variable region against carcinoembryonic antigen
 KW Carcinoembryonic antigen; immunogen; tumour; chimeric antibody.
 OS Murine (mouse) hybridoma CEM 231.6,7 (ATCC HB 9620).
 FH Key Location/Qualifiers
 FT CDS 1..324
 FT /*tag= a
 PN EP-332424-A.
 PD 13-SEP-1989.
 PF 08-MAR-1989; 302312.
 PR 09-MAR-1988; US-272577.
 PA (HYBR) Hybritech Inc.
 PI Beidler CB, Johnson MJ, Ludwig JR, Carlo DJ, David GS;
 DR WPI; 89-265635/37.
 DR P-PSDB; P91381.
 PT DNA constructs encoding light or heavy chain variable regions
 PT - chimeric monoclonal antibody, specific for human
 PT carcinoembryonic antigen, useful for diagnosis, imaging and
 PT treatment of tumours.
 PS Claim 2; page 18; 32pp; English.
 CC This region contained in a DNA construct with heavy chain variable
 CC and constant regions, light chain constant region, and 2 eukaryotic
 CC leader sequences. The chimeric monoclonal antibodies thus formed
 CC can be directed against CEA for immunoassay, and imaging and
 CC treatment of tumours, eg colorectal or breast carcinoma. The

constant regions are human-derived and so are less immunogenic
CC than entirely murine Abs.
SQ Sequence 324 BP; 85 A; 83 C; 77 G; 79 T;

Initial Score = 256 Optimized Score = 257 Significance = 18.60
Residue Identity = 80% Matches = 257 Mismatches = 61
Gaps = 0 Conservative Substitutions = 0

```
X      10      20      30      40      50      60      70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
|||||
GACATTGTGATGACCCAGTCTCAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAG
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
|||||
GCCAGTCAGAAATGTTCTGACTGCTGTTGCCTGGTATCAACAGAAACCAGGGCAGTCTCCTAAAGCACTGATT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
|||
TACTTGGCATCCAACCGGTACACTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACT
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCTCAGCAGGATTATAGCTCTCCGTAC
|||||
CTCACCATTACCAATGTGCAATCTGAAGACCTGGCAGATTATTTCTGTCTGCAACATTGGAATTATCCGCTC
     220     230     240     250     260     270     280

290      300      310      X
ACGTTCCGGAGGGGGGACCAAGCTGGAGATC
|||||
ACGTTCCGGTGTGGACCAAGCTGGAGCTGAAACGG
290      300      310      320
```

8. US-07-977-702-2 (1-318)

027132 Light chain variable region contg. ompA leader pep

ID 027132 standard; DNA; 387 BP.
AC 027132;
DT 21-JAN-1993 (first entry)
DE Light chain variable region contg. ompA leader peptide.
KW Heavy; antibody; Fv; CEM231.6.7; VL; ss; chelator.
OS Synthetic.
PN EP-497585-A.
PD 05-AUG-1992.
PF 30-JAN-1992; 300775.
PR 30-JAN-1991; US-647901.
PA (ANDE/) ANDERSON L D.
PA (COOK/) COOK J A.
PA (DAVI/) DAVID G S.
PA (HOCH/) HOCHSCHWENDER S M.
PA (KASH/) KASHER M S.
PA (SMIT/) SMITH M C.
PA (STEM/) STEMMER W P C.
PI Anderson LD, Cook JA, David GS, Hochschwender SM, Kasher MS;
PI Smith MC, Stemmer WPC;
DR WPI; 92-261005/32.
PT Immobilisation and purification of molecules - using kinetically
PT inert immobilised metal-CP-protein complex useful in assay
PT system
PS Example 5; Page 37; 88pp; English.

CC Sequencing of cloned CEH231.6.7. heavy and light chain variable
 CC regions along with the His-Trp-His-His-His fusion peptide was
 CC performed by standard procedures. This sequence shows the light
 CC chain variable sequence contg. the ompA leader peptide.
 CC See also Q27108-33.
 SQ Sequence 387 BP; 100 A; 100 C; 96 G; 91 T;

Initial Score = 256 Optimized Score = 257 Significance = 18.60
 Residue Identity = 80% Matches = 257 Mismatches = 61
 Gaps = 0 Conservative Substitutions = 0

```

                                X      10      20
                                AGTATTGTGATGACCCAGACTC
                                |||||
CTATCGGATCGCAGTGGCACTGGCTGGTTTCGCCACCGTGGCGCAGGCCGACATTGTGATGACCCAGTCTC
  20      30      40      50      60 X  70      80

      30      40      50      60      70      80      90
CCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
||||| || ||| ||||| ||||| ||| ||||| ||||| ||||| ||| |||
AAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGAATGTTCTGACTG
  90     100     110     120     130     140     150

      100     110     120     130     140     150     160
ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAAGCTGCTGATATATTATGCATCCAATCGCTACA
||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTGTTGCCTGGTATCAACAGAAACCAGGGCAGTCTCCTAAAGCACTGATTTACTTGGCATCCAACCGGTACA
 160     170     180     190     200     210     220

      170     180     190     200     210     220     230
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTGGAGTCCCTGATCGCTTCAACAGGCAGTGGATCTGGGACAGATTTCACTCTACCATTAACCAATGTGCAAT
 230     240     250     260     270     280     290     300

      240     250     260     270     280     290     300     310
CTGAAGACCTGGCAGTTTATTTCTGTCTGACAGGATTATAGCTCTCCGTACACGTTCCGAGGGGGACCAAGC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTGAAGACCTGGCAGATTATTTCTGTCTGCAACATTGGAATTATCCGCTCACGTTCCGGTGCTGGGACCAAGC
 310     320     330     340     350     360     370

      X
TGGAGATC
|||||
TGGAGCTGAAATAG
  380
  
```

9. US-07-977-702-2 (1-318)

Q28256 Fv heavy chain/light chain variable domain fusion

ID Q28256 standard; DNA; 748 BP.
 AC Q28256;
 DT 11-FEB-1993 (first entry)
 DE Fv heavy chain/light chain variable domain fusion protein.
 KW Minigene; pMZ18/1; monoclonal antibody; kappa; light chain;
 KW variable region; pMW31; tumour; ss.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT CDS 5..731
 FT /*tag= a
 FT misc_RNA 9..365
 FT /*tag= b
 FT /label= FRP5_heavy_chain_variable_domain
 FT misc_RNA 99..113
 FT /*tag= c

FT /label= CDR1H 156..206
 FT /*tag= d
 FT /label= CDR2H
 FT misc_RNA 303..332
 FT /*tag= e
 FT /label= CDR3H
 FT misc_RNA 366..410
 FT /*tag= f
 FT /label= Linker
 FT misc_RNA 411..728
 FT /*tag= g
 FT /label= FRP5_light_chain_variable_domain
 FT misc_RNA 480..512
 FT /*tag= h
 FT /label= CDR1L
 FT CDS 558..578
 FT /*tag= i
 FT /label= CDR2L
 FT misc_RNA 675..701
 FT /*tag= j
 FT /label= CDR3L
 PN EP-502812-A.
 PD 09-SEP-1992.
 PF 27-JAN-1992; 810056.
 PR 05-FEB-1991; EP-810079.
 PA (CIBA) CIBA GEIGY AG.
 PI Groner B, Hardman N, Harwerth I, Hynes NE, Wels WS;
 PI Zwickl M;
 DR MPI; 92-302096/37.
 DR P-PSDB; R26979.
 PT Recombinant antibodies directed to growth factor receptor C-erbB-2 -
 PT for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
 PT or ovarian tumours
 PS Disclosure; Page 31-33; 67pp; English.
 CC The sequence given encodes the Fv heavy chain/light chain variable
 CC domain fusion protein which binds to the extracellular domain of the
 CC growth factor receptor c-erbB-2. This recombinant antibody can be used
 CC for the qualitative and quantitative determination of c-erbB-2. This
 CC can be used for monitoring or in-vivo localisation of tumours
 CC overexpressing c-erbB-2.
 SQ Sequence 748 BP; 178 A; 190 C; 192 G; 188 T;

Initial Score = 256 Optimized Score = 259 Significance = 18.60
 Residue Identity = 81% Matches = 259 Mismatches = 59
 Gaps = 0 Conservative Substitutions = 0

```

                                X      10      20
                                AGTATTGTGATGACCCAGACTC
                                ||  | ||||| |||
CCTCTGGCGGTGGCGGTTCTGGTGGCGGTGGCTCCGGCGGTGGCGGTTCTGACATCCAGCTGACCCAGTCTC
  370      380      390      400      410      420      430

      30      40      50      60      70      80      90
CCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
||||| ||| ||||| ||||| ||| ||||| ||||| ||| |||||
ACAAATTCCTGTCCACTTCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGTATAATG
  440      450      460      470      480      490      500

      100      110      120      130      140      150      160
ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
||| || ||||| ||||| ||||| || ||||| ||||| ||| ||||| ||| |||||
CTGTGCGCTGTATCAACAGAAACCAGGACAATCTCCTAAACTTCTGATTTACTCGGCATCCTCCCGGTACA
  510      520      530      540      550      560      570

      170      180      190      200      210      220      230
  
```

CTGGAGTCCCTGATCCCTTCACCTGGCAGTGGATATGGGACGGATTTCACCTTCACCATCAGCAGTGTGCAGG
|||||
CTGGAGTCCCTTCTCGCTTCACTGGCAGTGGCTCTGGGCCGGATTTCACCTTCACCATCAGCAGTGTGCAGG
580 590 600 610 620 630 640

240 250 260 270 280 290 300 310
CTGAAGACCTGGCAGTTTATTCTGTGTCAGCAGGATTATAGCTCTCCGTACACGTTCCGAGGGGGACCAAGC
|||||
CTGAAGACCTGGCAGTTTATTCTGTGTCAGCAACATTTCTGTAAGTCCATTACGTTCCGCTCGGGGACAAAAT
650 660 670 680 690 700 710 720

X
TGGAGATC
|
TCGAGATCTAGCTGATCAAAGCTCTAGA
730 740

10. US-07-977-702-2 (1-318)
Q05557 Sequence encoding variable region of murine AHT 54

ID Q05557 standard; DNA; 411 BP.
AC Q05557;
DT 10-DEC-1990 (first entry)
DE Sequence encoding variable region of murine AHT 54 light chain.
KW Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 58..411
FT /*tag= a
PN EP-380068-A.
PD 01-AUG-1990.
PF 24-JAN-1990; 101351.
PR 24-JAN-1989; US-301216.
PR 04-DEC-1989; US-441702.
PA (MOLE-) MOLECULAR THERAPEU.
PI Zerler B;
DR WPI; 90-232892/31.
DR P-PSDB; R06253.
PT Expression vectors for producing chimeric monoclonal antibodies -
PT which express human constant region and non-human variable region
PS Disclosure; p; English.
CC MAbs comprising mouse CH and CL constant regions with human
CC variable regions may be used to create mouse/human hybrid MAbs,
CC which have a longer serum half-life. Method can be used to produce
CC Abs against interleukin-2 receptor and tumour necrosis factor.
SQ Sequence 411 BP; 110 A; 94 C; 104 G; 103 T;

Initial Score = 255 Optimized Score = 259 Significance = 18.52
Residue Identity = 81% Matches = 260 Mismatches = 58
Gaps = 1 Conservative Substitutions = 0

X 10 20
AG-TATTGTGATGACCCAGACT
||
CAGACTCAGGTCTTTGTATACATGTTGCTGTGGTTGTCTGGTGGTGATGGAGACATTGTGATGACCCAGTCT
40 50 60 70 80 X 90 100

30 40 50 60 70 80 90
CCCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAAT
| ||||| || |||| ||||| || || ||||| ||||| |||| ||
CAAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGTCACCTGCAAGGCCAGTCAGAATGTGGGTACT
110 120 130 140 150 160 170 180

100 110 120 130 140 150 160
GATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTAC

```

310          X
CTGGAGATC
||||| |||
CTGGAAATCAAACGG
400          X 410

```

11. US-07-977-702-2 (1-318)

N40022 cDNA insert of pK17G4 encoding kappa anti-carcinome

ID N40022 standard; cDNA; 882 BP.
AC N40022;
DT 01-DEC-1991 (first entry)
DE cDNA insert of pK17G4 encoding kappa anti-carcinoembryonic antigen.
KW Immunoglobulin; ds DNA; carcinoembryonic antigen; vector pK17G4.
PN EP-125023-A.
PD 14-NOV-1984.
PF 06-APR-1984; 302368.
PR 08-APR-1983; US-483457.
PA (CITY) City of Hope.
PA (GETH) Genentech Inc.
PI Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD.
DR WPI; 84-283749/46.
PT Immunoglobulin(s) produced by recombinant host cells - useful as
PT antibodies analogous to forms from mammals.
PS Disclosure; Fig. 2A-B; 79pp; English.
CC The cDNA is contained within recombinant vector pK17G4 and encodes
CC kappa anti-carcinoembryonic antigen chain. Using the vector the
CC immunoglobulin is produced readily in pure monoclonal form. Genetic
CC manipulations can be used to produce chimeras of variants drawing
CC their homology from species differing from each other. Protein
CC manipulation is also possible.
SQ Sequence 882 BP; 231 A; 243 C; 194 G; 214 T;

Initial Score	=	252	Optimized Score	=	254	Significance	=	18.29
Residue Identity	=	79%	Matches	=	255	Mismatches	=	63
Gaps	=	1	Conservative Substitutions	=	0			

50 60 70 80 90 100 110
 AGGAGACAGGGTTACCATAACCTGCAGGCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAA
 |||||
 AGGAGACAGGGTCAGCATCACCTGCAGGCCAGTCAGGATGTGGTGCTGCTATAGCCTGGTATCAACAGAA
 80 90 100 110 120 130 140

```

120      130      140      150      160      170      180      190      200      210
GCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCAC
||||| || ||||| ||||| ||| ||||| || ||||| ||||| ||||| ||||| |||||
ACCAGGACAATCTCCTAAACTACTGATTTACTGGGCATCCACCGGCACACTGGAGTCCCTGATCGCTTCAC
150      160      170      180      190      200      210

190      200      210      220      230      240      250      260
TGGCAGTGGATATGGGACGGATTTCACTTTTACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATT
||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AGGCACTGGATCTGGGACAGATTTCACTCTCACCATTAGCAATGTGCAGTCTGATGACTTGGCAGATTATT
220      230      240      250      260      270      280

270      280      290      300      310      X
CTGTCAACAGATTATAGCTCTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAGATC
||||| || || || ||| ||||| || ||||| ||||| ||||| ||||| |||||
CTGTCAACAATATAGCGGTATCCTCTCACGTTCCGTGCTGGGACCAAGCTGGAGCTGAAACGGGCTGATGC
290      300      310      320      330      340      X 350      360

TGCACCAACTGTATCCATCTTCCCACCATCCAGTGA
370      380      390

```

12. US-07-977-702-2 (1-318)

004264 Encodes Colon Cancer monoclonal antibody CC83 ligh

ID 004264 standard; DNA; 685 BP.
AC 004264;
DT 13-SEP-1990 (first entry)
DE Encodes Colon Cancer monoclonal antibody CC83 light chain variable region
KW chimeric antibodies; TAG72; light chain variable region;
KW heavy chain variable region; ss
OS synthetic.
FH Key Location/Qualifiers
FT intron 136..313
FT /*tag= a
FT transit_peptide 76..325
FT /*tag= b
FT /note="intron is spliced out"
FT misc_feature 326..610
FT /*tag= c
FT /label= encodes variable segment
FT misc_feature 611..646
FT /*tag= d
FT /label=encodes J4 segment
PN EP-365997-A.
PD 02-MAY-1990.
PF 18-OCT-1989; 119361.
PR 19-OCT-1988;US-259943.
PA (DOWC) Dow Chemical Co.
PI Mezes P, Gourlie B, Rixon M;
DR WPI; 90-133521/18.
DR P-PSDB; R04387.
PT Chimeric antibodies against TAG72 and conjugate to provide imaging
PT markers and therapeutic tools
PS Disclosure; pp; English.
CC The polypeptide encoded by this sequence forms part of a chimera. The
CC other components are a heavy chain variable region and human-derived
CC constant light and heavy chain regions. The variable regions have
CC high affinity for TAG72. The constant regions reduce the side-effects
CC when administered to human patients because they are of human origin.
CC See also 004258-63 and 004265-9.
SQ Sequence 685 BP; 187 A; 138 C; 153 G; 207 T;

Initial Score = 250 Optimized Score = 253 Significance = 18.13
Residue Identity = 79% Matches = 254 Mismatches = 64
Gaps = 1 Conservative Substitutions = 0

```

X      10      20
AG-TATTGTGATGACCCAGACT
|| |||||
TATGTGTGAGTTTATACACATTATCTGTTTCTGTTTGCAGGTGTTGAAGGAGACATTGTGATGACCCAGTCT
280      290      300      310      320      X 330      340

      30      40      50      60      70      80      90
CCCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAAT
| ||||| || | |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CACAAATTCATGTCCGCATCAGTGGGAGACAGGGTCAACATCACCTGCAAGGCCAGTCAGTATGTGGCTACT
350      360      370      380      390      400      410

      100      110      120      130      140      150      160
GATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTAC
| ||||| |||| | || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GCTGTAGCCTGGTTTCAGCATAAACCAGGTCAGTCTCCTAAACTACTGATTACGGGGCATCCACCCGGCAC
420      430      440      450      460      470      480      490

      170      180      190      200      210      220      230
ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ACTGGAGTCCCTGATCGCTTCAACGGCAGTGGATCTGGGACAGATTTCACTCTCATCATTAGCAATGTGCAG
500      510      520      530      540      550      560

      240      250      260      270      280      290      300
GCTGAAGACCTGGCAGTTTATTTCTGTCTCAGCAGGATTATAGCTCTCCGTACACGTTTCGGAGGGGGACCAAG
|||| || ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
TCTGAGGACTTGGCAGATTATTTGTGTCTCAGCATTATAGCGGCTATCCATTACGTTTCGGGCTCGGGGACAAAG
570      580      590      600      610      620      630

310      X
CTGGAGATC
|||| ||
TTGGAATAAAACGTAAGTAGACTTTTGCTCATTTACTTGTGACGTTTTGG
640      X 650      660      670      680

```

13. US-07-977-702-2 (1-318)

N40023 mRNA encoding kappa anti-carcinoembryonic antigen.

ID N40023 standard; mRNA; 882 BP.
AC N40023;
DT 01-DEC-1991 (first entry)
DE mRNA encoding kappa anti-carcinoembryonic antigen.
KW Immunoglobulin; ss mRNA; carcinoembryonic antigen.
FH Key Location/Qualifiers
FT CDS 1..673
FT /*tag= a
PN EP-125023-A.
PD 14-NDV-1984.
PF 06-APR-1984; 302368.
PR 08-APR-1983; US-483457.
PA (CITY) City of Hope.
PA (GETH) Genentech Inc.
PI Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD.
DR MPI; 84-283749/46.
DR P-PSDB; P40031.
PT Immunoglobulin(s) produced by recombinant host cells - useful as
PT antibodies analogous to forms from mammals.
PS Disclosure; Fig. 3; 79pp; English.
CC The mRNA is the coding sequence of the cDNA fragment contained within
CC recombinant vector pK17G4 (see N40022). It encodes kappa anti-
CC carcinoembryonic antigen chain. Using the vector the immunoglobulin is
CC produced readily in pure monoclonal form. Genetic manipulations can be
CC used to produce chimeras of variants drawing their homology from species

CC differing from each other. Protein Manipulation is also possible.
SQ Sequence 882 BP; 231 A; 244 C; 194 G; 213 U;

Initial Score = 249 Optimized Score = 253 Significance = 18.06
Residue Identity = 59% Matches = 254 Mismatches = 64
Gaps = 1 Conservative Substitutions = 0

```

      X      10      20      30      40
      AG-TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTCAGC
      || ||||| ||||| || ||||| || |||||
GUUGCUGUGGUUGUCUGGUGUUGAAGGAGACAUUGUGAUGACCCAGUCACAAUUAUGUCCACAUCAGU
      10      20      30      40      50      60      70

      50      60      70      80      90      100     110
AGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAA
||||| ||||| || ||||| ||||| ||||| || || ||||| ||||| ||||| |||||
AGGAGACAGGGUCAGCAUACCUGCAAGGCCAGUCAGGAUGUGGGUGCUGCUAUAGCCUGGUAUACAACAGAA
      80      90      100     110     120     130     140

      120     130     140     150     160     170     180
GCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCAC
||||| || ||||| ||||| || || ||||| || ||||| ||||| ||||| |||||
ACCAGACAAUUCUCAAACUACUGAUUUACUGGGCAUCCACCCGGCACACUGGAGUCCUGAUCGCUUCAC
      150     160     170     180     190     200     210

      190     200     210     220     230     240     250     260
TGGCAGTGGATATGGGACGGATTTCACTTTACCATCAGCACTGTGTCAGGCTGAAGACCTGGCAGTTATTT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AGGCAGUGGAUCUGGGACAGAUUUCACUCACCAUUAAGCAAUGUGCAGUCUGAUGACUUGGCAGAUUAUUU
      220     230     240     250     260     270     280

      270     280     290     300     310     X
CTGTCAGCAGGATTATAGCTCTCCGTACACGTTCCGGAGGGGGACCAAGCTGGAGATC
||||| || || || ||||| || ||||| ||||| ||||| ||||| || ||
CUGUCAACAAUUAAGCGGGUAUCCUCUCACGUUCGGUGCGGGACCAAGCUGCAGCUGAAACGGGCUGAUGC
      290     300     310     320     330     340     X 350     360

      UGCACCAACUGUAUCCAUCUCCACCAGCCAGUGA
      370     380     390
```

14. US-07-977-702-2 (1-318)
Q25592 Encodes 4D5 Fab IgG antibody - recognises HER-2 re

ID Q25592 standard; DNA; 2178 BP.
AC Q25592;
DT 08-DEC-1992 (first entry)
DE Encodes 4D5 Fab IgG antibody - recognises HER-2 receptor.
KW humanised IgG antibody; human growth hormone; hGH; selection;
KW screening; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT exon 1..712
FT /*tag= a
FT /product= light chain
FT exon 796..2178
FT /*tag= b
FT /product= heavy chain
PN W09209690-A.
PD 11-JUN-1992.
PF 03-DEC-1991; U09133.
PR 03-DEC-1990; US-621667.
PR 10-APR-1991; US-683400.
PR 14-JUN-1991; US-715300.
PR 08-AUG-1991; US-743614.
PA (GETH) GENENTECH INC.

PI Bass S; Garrard LV; Greene R; Henner DJ; Lowman HB;
 DR WPI: 92-217069/26.
 DR P-PSDB: R24047.8.
 PT Selecting and enriching variant proteins - comprises fusing gene
 PT encoding e.g. growth hormone to part of M13 phage coat protein
 PT and mutagenising fusion prior to selection
 PS Claim 46; Fig 11; 102pp; English.
 CC This sequence encodes the Fab portion of the 4D5 humanised IgG
 CC antibody that recognises the HER-2 receptor. It was inserted into
 CC the plasmid pS0132, which had the DNA encoding human growth hormone
 CC excised from it. The plasmid was used to transform E. coli SR101.
 CC The sequence encodes two genes. The first encodes the variable and
 CC constant regions of the light chain, and with the st II signal
 CC sequence at its 5' end. The second contains four regions - the st II
 CC signal sequence at its 5' end, the variable domain of the heavy chain,
 CC the first domain of the heavy chain constant region, followed by the
 CC M13 gene III.
 SQ Sequence 2178 BP; 498 A; 572 C; 549 G; 559 T;

Initial Score = 234 Optimized Score = 237 Significance = 16.89
 Residue Identity = 74% Matches = 237 Mismatches = 81
 Gaps = 0 Conservative Substitutions = 0

```

                                X      10      20
                                AGTATTGTGATGACCCAGACTC
                                ||| |||||
TTCTTCTTGCATCTATGTTTCGTTTTTCTATTGCTACAAACGGTACGCTGATATCCAGATGACCCAGTCCC
20      30      40      50      60      70      80      90

      30      40      50      60      70      80      90
CCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
| | | ||| | | | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
CGAGCTCCCTGTCCGCCTCTGTGGCGATAGGGTCACCATCACCTGCCGTGCCAGTCAGGATGTGAATACTG
100     110     120     130     140     150     160

      100     110     120     130     140     150     160
ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
||||| ||||| ||||| ||||| | |||| |||| |||| || | ||||| | ||||
CTGTAGCCTGGTATCAACAGAAACAGGAAAAGCTCCGAAACTACTGATTTACTCGGCATCCTTCCTCTACT
170     180     190     200     210     220     230

      170     180     190     200     210     220     230
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
||||||| ||||| |||| ||| ||||| ||||| ||| ||||| ||| |||||
CTGGAGTCCCTTCTCGCTTCTGTGGATCCAGATCTGGGACGGATTTCACTCTGACCATCAGCAGTCTGCAGC
240     250     260     270     280     290     300

240     250     260     270     280     290     300     310
CTGAAGACCTGGCAGTTTATTTCTGTGAGGATTATAGTCTCCGTACACGTTCCGAGGGGGACCAAGC
| ||||| | ||| ||||| ||||| ||||| |||| ||||| ||| |||||
CGGAAGACTTCGCAACTTATTACTGTGAGCAACATTATACTACTCTCCACGTTCCGACAGGGTACCAAGG
310     320     330     340     350     360     370

```

```

      X
      TGGAGATC
      |||||
      TGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
380     390     400     410     420     430

```

15. US-07-977-702-2 (1-318)
 Q28747 Anti-CEA specific light chain variable region DNA.

ID Q28747 standard; DNA; 387 BP.
 AC Q28747;

DT 01-MAR-1993 (first entry)
 DE Anti-CEA specific light chain variable region DNA.
 KW Human; carcinoembryonic antigen; heavy chain; light chain; variable;
 KW region; diagnostic; tumour; markers; targetting; ss.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT sig_peptide 1..60
 FT /*tag= a
 FT mat_peptide 61..387
 FT /*tag= b
 PN J04234987-A.
 PD 24-AUG-1992.
 PF 28-DEC-1990; 408810.
 PR 28-DEC-1990; JP-408810.
 PA (MITU) MITSUBISHI KASEI CORP.
 DR WPI; 92-327631/40.
 DR P-PSDB; R27054.
 PT New DNA fragments encoding variable regions of ABS specific for
 PT human CEA - for diagnosing and monitoring tumours, as tumour
 PT markers and for treatment of tumours
 PS Claim 1; Fig 2; 7pp; Japanese.
 CC The anti-CEA murine monoclonal antibody light chain variable region
 CC was obtd. by screening a cDNA library prepd. from mRNA obtd. from
 CC hybridomas producing anti-CEA-specific antibodies with a probe
 CC based on the constant region of the L-chain. The antibodies reacts
 CC specifically with human CEA and are useful as a diagnostic agents,
 CC as tumour markers for digestive organs, for diagnosis of malignant
 CC tumours; for monitering after cancer operations, to follow up bloodless
 CC therapy or as therapeutic agents in passive immune therapy and
 CC targetting therapy. See also 028744-6.
 SQ Sequence 387 BP; 105 A; 92 C; 95 G; 95 T;

Initial Score = 227 Optimized Score = 257 Significance = 16.34
 Residue Identity = 80% Matches = 260 Mismatches = 58
 Gaps = 4 Conservative Substitutions = 0

```

                                X      10      20
                                AG-TATTGTGATGACCCAGACT
                                || ||||| ||||| ||
CAGACTCAGGTCTTTCTATACATCTTGCTGTGGTTGTCTGGTGTGATGGAGACATTGTGATGACCCAGTCT
10      20      30      40      50      60      70      80

      30      40      50      60      70      80      90
CCCAAATTCCTGCTTGTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAAT
| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGTCACCTGCAAGGCCAGTCAGAATGTGGGTACT
90      100     110     120     130     140     150

      100     110     120     130     140     150     160
GATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTGCATCCAATCGCTAC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AATGTAGCCTGGTATCAACAGAAACCAGGGCAATCTCCTAAAGCACTGATTAACCTCGGCATCTACCGGTAC
160     170     180     190     200     210     220

      170     180     190     200     210     220     230
ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACCTTCACCATCAGCACTGTGCAG
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AGTGGAGTCCCTGATCGCTTCAACAGCAGTGGATCTGGGACAGATTTCACCTCTACCATCAGCAATGTGCGG
230     240     250     260     270     280     290

      240     250     260     270     280     290     300
GCTGAAGACCTGGCAGTTTATTTCTGTCTCAGCAGGATTATAGCT---CTCCGTACACGTTCCGAGGGGGACC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TCTGAAGACTTGGCAGAGTATTTCTGTCTCAGCAATATAACAGCTATCCTCTCTACACATTCCGAGGGGGCACC
300     310     320     330     340     350     360
  
```

310
 AAGCTGGAGATC
 || ||||| ||
 AACCTGGAAATAAAACGG
 370 380

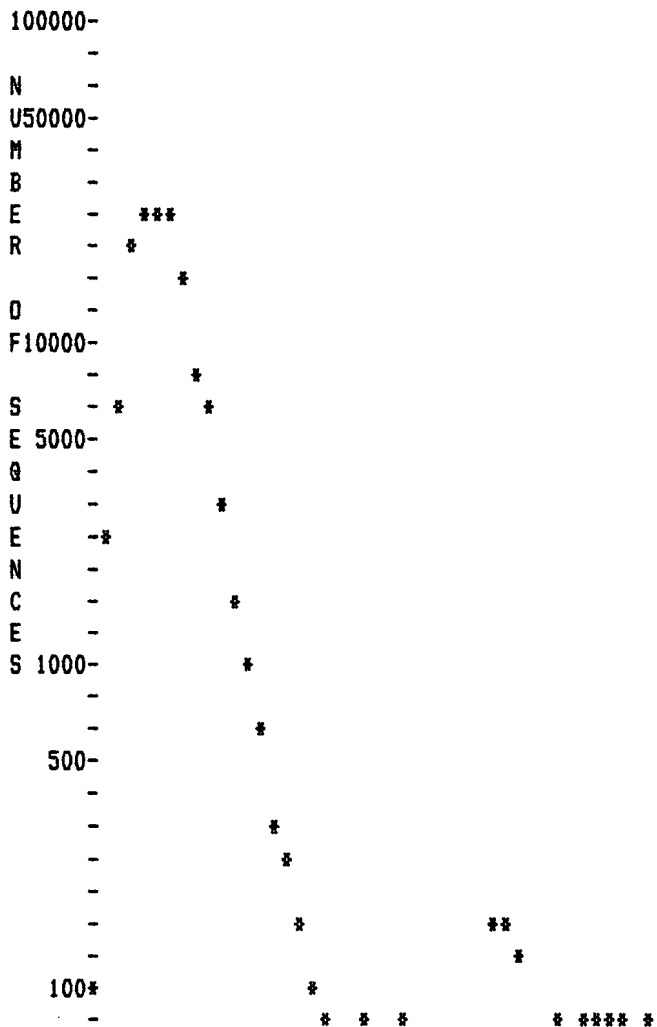
> 0 <
 0| 0 IntelliGenetics
 > 0 <

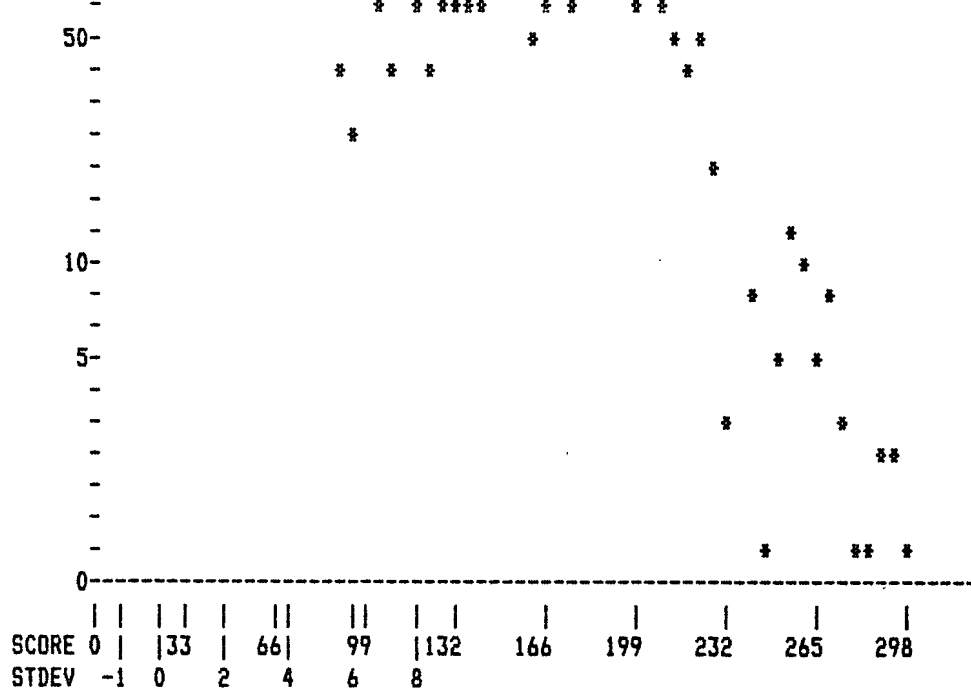
FastDB - Fast Pairwise Comparison of Sequences
 Release 5.4

Results file us-07-977-702-2.res made by shears on Tue 15 Jun 93 11:04:41-PDT.

Query sequence being compared:US-07-977-702-2 (1-318)
 Number of sequences searched: 125798
 Number of scores above cutoff: 4066

Results of the initial comparison of US-07-977-702-2 (1-318) with:
 Data bank : EMBL-NEW 3, all entries
 Data bank : GenBank 75, all entries
 Data bank : GenBank-NEW 3, all entries
 Data bank : UEMBL 34_75, all entries





PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	1.00	Window size	32
Gap size penalty	0.33		
Cutoff score	0		
Randomization group	0		

Initial scores to save	40	Alignments to save	15
Optimized scores to save	0	Display context	50

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	27	27	11.35

Times:	CPU	Total Elapsed
	00:28:23.05	00:58:37.00

Number of residues:	150464018
Number of sequences searched:	125798
Number of scores above cutoff:	4066

Cut-off raised to 21.
 Cut-off raised to 26.
 Cut-off raised to 29.
 Cut-off raised to 32.
 Cut-off raised to 34.
 Cut-off raised to 36.
 Cut-off raised to 39.
 Cut-off raised to 41.
 Cut-off raised to 43.
 Cut-off raised to 46.
 Cut-off raised to 49.
 Cut-off raised to 52.
 Cut-off raised to 56.

The scores below are sorted by initial score.
 Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt. Score	Sig.	Frame
**** 23 standard deviations above mean ****						
1. MUSOHP57K	Mus musculus mRNA for Ig kapp	322	298	300	23.87	0
2. S63304	Vk28 VkJk [not specified, Gen	322	295	297	23.61	0
3. MUSSCETK	Mus musculus DNA for Ig kappa	322	295	297	23.61	0
4. MMIGRF28	Murine MRL-RF28L mRNA for IgM	398	295	298	23.61	0
5. MUSIGKCPF	Mouse Ig active kappa-chain (938	290	293	23.17	0
6. MMIGKL	Mouse mRNA for Ig C.C58 M75 k	938	290	293	23.17	0
**** 22 standard deviations above mean ****						
7. S60946	mAb BA.N4:4.57 V kappa region	300	287	289	22.91	0
8. MMVL105	Mouse mRNA for kappa-immunogl	321	287	290	22.91	0
9. MUSIGKVM	Mouse Ig germline kappa-chain	1816	280	294	22.29	0
10. S60873	Ab2 kappa chain V region mA	300	278	279	22.11	0
**** 21 standard deviations above mean ****						
11. MMNPCRLB6	M.musculus NPCRLB6 mRNA for i	321	273	275	21.67	0
12. MUSIGKCNK	Mouse Ig rearranged kappa-cha	456	272	275	21.58	0
13. MMNPCRLB1	M.musculus NPCRLB1 mRNA for i	321	271	273	21.50	0
14. MUSIGKVN	Mouse Ig germline kappa-chain	2002	270	284	21.41	0
15. MUSIGKCKP	Mouse Ig kappa-chain mRNA V-r	341	269	272	21.32	0
16. MUSIGLAFF	Mouse Ig kappa-chain mRNA V r	318	268	271	21.23	0
17. S51704	hybridoma antibody kappa-chai	313	266	266	21.06	0
18. MUSIGKAF0	Mouse Ig active kappa-chain m	313	266	266	21.06	0
19. MUSIGLAFD	Mouse Ig kappa-chain mRNA V r	315	266	266	21.06	0
20. MUSIGKAL	Mouse Ig active kappa gene: M	739	266	269	21.06	0
**** 20 standard deviations above mean ****						
21. MMVL3190	Mouse mRNA for kappa-immunogl	321	264	264	20.88	0
22. MUSIGKCSR	Mouse Ig active kappa-chain m	321	262	265	20.70	0
23. MUSIGKAAV	Mouse Ig rearranged kappa-cha	363	262	270	20.70	0
24. MUSIGKAQ	Mouse Ig kappa active gene: k	765	261	263	20.61	0
25. S51746	hybridoma antibody kappa-chai	276	260	261	20.53	0
26. MUSIGKAFV	Mouse Ig active kappa-chain m	275	259	260	20.44	0
27. MMBV1745L	M.musculus light chain variab	324	259	261	20.44	0
28. MUSIGKAJ	mouse ig kappa mrna from mopc	943	259	262	20.44	0
29. MMIGK9	Messenger RNA for mouse immun	943	259	262	20.44	0
30. MUSIGKAJA	Mouse Ig kappa active mRNA fr	462	258	261	20.35	0
31. MUSNC41	Mus musculus NC41 mRNA, parti	324	257	260	20.26	0
32. MMIGKV	Mouse mRNA for immunoglobulin	462	257	259	20.26	0
33. M245877S1	anti-human erbB-2 receptor bi	894	257	260	20.26	0
34. MUSIGKAED	Mouse Ig active kappa chain m	321	256	258	20.17	0
35. MUSIGLAA	Mouse rearranged light chain	354	256	260	20.17	0
36. HUMIGLIA	Human Ig light chain VJ regio	618	256	258	20.17	0
37. S115039	immunoglobulin light chain va	411	255	259	20.09	0
**** 19 standard deviations above mean ****						
38. MUSIGKCNM	Mouse Ig active kappa chain m	321	254	259	20.00	0
39. MUSIGLAB	Mouse rearranged light chain	357	254	260	20.00	0
40. MUSIGLAFE	Mouse Ig kappa-chain mRNA V r	303	253	257	19.91	0

1. US-07-977-702-2 (1-318)

MUSOHP57K Mus musculus mRNA for Ig kappa chain precursor.

LOCUS MUSOHP57K 322 bp ss-mRNA ROD 11-NOV-1992
 DEFINITION Mus musculus mRNA for Ig kappa chain precursor.
 ACCESSION D12733
 KEYWORDS Ig kappa chain; steroid specific antibody; variable region.
 SOURCE Mus musculus (strain BALB/c) hybridoma cell line OHP57.G6.1 mRNA.
 ORGANISM Mus musculus
 Eukaryota; Animalia; Chordata; Mammalia; Rodentia; Muridae.
 REFERENCE 1 (bases 1 to 322)
 AUTHORS Sawada,J., Mizusawa,S., Terao,T., Naito,M. and Kurosawa,Y.

TITLE Molecular characterization of monoclonal anti-steroid antibodies:
 primary structures of the variable regions of seven antibodies
 specific for 17alpha-hydroxyprogesterone or 11-deoxycortisol and
 their pH-reactivity profiles
 JOURNAL Mol. Immunol. 28, 1063-1072 (1991)
 STANDARD full automatic
 COMMENT Submitted (27-JUL-1992) to DDBJ by: Jun-ichi Sawada
 Dept. of Biochem. and Immunochem.
 National Institute of Hygienic Sciences
 1-18-1 Kamiyoga
 Setagaya, Tokyo 158
 Japan
 Phone: 03-3700-1141 x240
 Fax: 03-3707-6950.
 FEATURES Location/Qualifiers
 mat_peptide 1..>322
 /product="Ig kappa chain"
 /codon_start=1
 /note="VJ region (1-322)"
 CDS <1..>322
 /product="Ig kappa chain precursor"
 /codon_start=1
 /translation="SIVMTQTPKFLIRAGDRVMTCKASQ SARNGVAVYQKPGQSP
 KLLIYYTSDRYTGVPDRFTGSGYGTDFFTISTVQ AEDVAVYFCQVYSSPYTFGGGT
 KLEIK"
 BASE COUNT 86 a 76 c 84 g 76 t
 ORIGIN

Initial Score = 298 Optimized Score = 300 Significance = 23.87
 Residue Identity = 94% Matches = 300 Mismatches = 18
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
|||||
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTATAAGAGCAGGAGACAGGGTCACCATGACCTGCAAG
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
|||||
GCCAGTCAGAGTGGCGAAATGGTGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
|| |||
TACTATACATCCGATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTGACAGGATTATAGCTCTCCGTAC
|||||
TTCACCATCAGCACTGTGCAGGCTGAAGACGTGGCAGTTTATTTCTGTGACAGGTTATAGTTCTCCGTAC
     220     230     240     250     260     270     280

290      300      310      X
ACGTTCCGGAGGGGGACCAAGCTGGAGATC
|||||
ACGTTCCGGAGGGGGACCAAGCTGGAATAAAAC
290      300      310      320
  
```

2. US-07-977-702-2 (1-318)

S63304 Vk28 VkJk [not specified, Genomic, 322 nt]

LOCUS S63304 322 bp DNA 03-JAN-1992
 DEFINITION Vk28 VkJk [not specified, Genomic, 322 nt]
 ACCESSION S63304
 KEYWORDS .
 SOURCE not specified
 ORGANISM Unclassified.
 Unclassified.
 REFERENCE 1 (bases 1 to 322)
 AUTHORS Sawada,J., Mizusawa,S., Terao,T., Naito,M. and Kurosawa,Y.
 TITLE Molecular characterization of monoclonal anti-steroid antibodies:
 primary structures of the variable regions of seven antibodies
 specific for 17 alpha-hydroxyprogesterone or 11-deoxycortisol and
 their pH-reactivity profiles.
 JOURNAL Mol. Immunol. 28, 1063-1072 (1991)
 STANDARD full automatic
 COMMENT This entry [NCBI gibbsq 63304] was created by the journal scanning
 component of NCBI/GenBank at the National Library of Medicine.
 This sequence comes from Fig 5.
 FEATURES
 CDS Location/Qualifiers
 1..322
 /partial
 /note="Description: Vk28 VkJk; kappa chain variable and
 joining region; For the protein sequence (NCBI gibbsq
 63309): Method: conceptual translation with partial
 peptide sequencing. This sequence comes from Fig 6."
 /product="monoclonal antibody SCET.M8.1"
 /codon_start=1
 /translation="SIVMTQTPKFLHVSVGDRVTITCKASQSVRNAVVWYQ@KTGLSP
 RLLIYYASNRYTGVPRDTFGSGYGTDFLTIRSVAEEDLAVYFCQ@NFKSPYTFGGGT
 KLEIK"
 BASE COUNT 87 a 72 c 84 g 79 t
 ORIGIN

Initial Score = 295 Optimized Score = 297 Significance = 23.61
 Residue Identity = 93% Matches = 297 Mismatches = 21
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
|||||
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTGATGATCAGTAGGAGACAGGGTTACCATAACCTGCAAG
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
|||||
GCCAGTCAGAGTGTGAGGAATGCTGTAGTTTGGTACCAACAGAAGACAGGGCTGTCTCCTAGACTGCTGATA
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
|| |||||
TACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTGACAGGATTATAGCTCTCCGTAC
|||||
CTCACCATCAGAAGTGTGGAGGCTGAAGACCTGGCAGTTTATTTCTGTGACAGAAATTTAAGTCTCCGTAC
     220     230     240     250     260     270     280

     290     300     310     X
ACGTTCGGAGGGGGGACCAAGCTGGAGATC
|||||
ACGTTCGGAGGGGGGACCAAGCTGGAATAAAAC
     290     300     310     320

```

3. US-07-977-702-2 (1-318)

MUSSCETK Mus musculus DNA for Ig kappa chain precursor.

LOCUS MUSSCETK 322 bp ds-DNA ROD 11-NOV-1992
 DEFINITION Mus musculus DNA for Ig kappa chain precursor.
 ACCESSION D12737
 KEYWORDS Ig kappa chain; steroid specific antibody; variable region.
 SOURCE Mus musculus (strain BALB/c) hybridoma cell line SCET.M8.1.1 DNA.
 ORGANISM Mus musculus
 Eukaryota; Animalia; Chordata; Mammalia; Rodentia; Muridae.
 REFERENCE 1 (bases 1 to 322)
 AUTHORS Sawada,J., Mizusawa,S., Terao,T., Naito,M. and Kurosawa,Y.
 TITLE Molecular characterization of monoclonal anti-steroid antibodies:
 primary structures of the variable regions of seven antibodies
 specific for 17alpha-hydroxyprogesterone or 11-deoxycortisol and
 their pH-reactivity profiles
 JOURNAL Mol. Immunol. 28, 1063-1072 (1991)
 STANDARD full automatic
 FEATURES Location/Qualifiers
 mat_peptide 1..>322
 /product="Ig kappa chain"
 /codon_start=1
 /note="VJ region (1-322)"
 CDS <1..>322
 /product="Ig kappa chain precursor"
 /codon_start=1
 /translation="SIVMTQTPKFLHVSVDRTITCKASQSVRNAVVWYQQTGLSP
 RLLIYYASNRYTGVPDRFTGSGYGTDFLTIRSVAEADLAVYFCQNFKSPYTFGGGT
 KLEIK"
 BASE COUNT 87 a 72 c 84 g 79 t
 ORIGIN

Initial Score = 295 Optimized Score = 297 Significance = 23.61
 Residue Identity = 93% Matches = 297 Mismatches = 21
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
|||||
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTGATGATCAGTAGGAGACAGGGTTACCATAACCTGCAAG
X      10      20      30      40      50      60      70

```

```

      80      90     100     110     120     130     140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
|||||
GCCAGTCAGAGTGTGAGGAATGCTGTAGTTTGGTACCAACAGAAGACAGGGCTGTCTCCTAGACTGCTGATA
      80      90     100     110     120     130     140

```

```

     150     160     170     180     190     200     210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
||
TACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
     150     160     170     180     190     200     210

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     220     230     240     250     260     270     280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTGACAGGATTATAGCTCTCCGTAC
|||||
CTCACCATCAGAAGTGTGGAGGCTGAAGACCTGGCAGTTTATTTCTGTGACAGAAATTTAAGTCTCCGTAC
     220     230     240     250     260     270     280

```

```

290      300      310      X
ACGTTCTGGAGGGGGACCAAGCTGGAGATC
|||||
ACGTTCTGGAGGGGGACCAAGCTGGAAATAAAC

```

4. US-07-977-702-2 (1-318)

MMIGRF28 Murine MRL-RF28L mRNA for IgM (kappa)-light chain

LOCUS MMIGRF28 398 bp RNA ROD 04-AUG-1992
 DEFINITION Murine MRL-RF28L mRNA for IgM (kappa)-light chain V(kappa)28, J(kappa) 1
 ACCESSION X14622
 KEYWORDS autoantibody; Ig kappa light chain; Ig light chain; IgM; immunoglobulin; variable region.
 SOURCE mouse
 ORGANISM Mus musculus
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 398)
 AUTHORS Kofler, R.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAR-1989) Kofler R., General and Experimental Pathology, University of Innsbruck, Fritz-Pregl-Str.3, A-6020 Innsbruck, Austria.
 STANDARD full automatic
 REFERENCE 2 (bases 1 to 362)
 AUTHORS Kofler, R., Duchosal, M.A. and Dixon, F.J.
 TITLE Complexity, polymorphism, and connectivity of mouse V-kappa gene families
 JOURNAL Immunogenetics 29, 65-74 (1989)
 STANDARD full automatic
 COMMENT *source: strain=MRL/Mp-lpr/lpr;
 *source: haplotype=Ig(kappa)(a);
 *source: tissue=spleen;
 *source: cell_type=hybridoma;
 *source: cell_line=MRL-RF28;
 Data kindly reviewed (24-jul-1989) by Kofler R.
 FEATURES
 CDS
 18..>398
 /note="IgM; (kappa)-light chain precursor"
 /codon_start=1
 /translation="MKSQTQVFIFLLLCVSGAHGSIVMTQTPKFLPVSAGDRVMTCK
 ASQSVGNVAVYQQKPGQSPKLLIYYASNRYTCVPDRFTGSGSGTDFTFTISSVQVED
 LAVYFCQQHYSSPWTFGGGTKLEIK"
 CDS
 18..77
 /note="signal peptide; (AA -20 to -1)"
 /codon_start=1
 /translation="MKSQTQVFIFLLLCVSGAHG"
 CDS
 78..>398
 /note="mature IgM; (kappa)-light chain (AA 1-107)"
 /codon_start=1
 /translation="SIVMTQTPKFLPVSAGDRVMTCKASQSVGNVAVYQQKPGQSP
 KLLIYYASNRYTCVPDRFTGSGSGTDFTFTISSVQVEDLAVYFCQQHYSSPWTFGGGT
 KLEIK"
 BASE COUNT 102 a 97 c 100 g 99 t
 ORIGIN
 Initial Score = 295 Optimized Score = 298 Significance = 23.61
 Residue Identity = 93% Matches = 298 Mismatches = 20
 Gaps = 0 Conservative Substitutions = 0

X 10 20
 AGTATTGTGATGACCCAGACTC
 |||||
 AGACCCAGGTCTTCATATTTCTACTGCTCTGTGTCTGGTGCTCATGGGAGTATTGTGATGACCCAGACTC
 30 40 50 60 70 80 90


```

      30      40      50      60      70      80      90
CCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CCAAATTCCTGCTGTATCAGCAGGAGACAGGGTTACCATGACCTGCAAGGCCAGTCAGAGTGTGGGTAATA
100      110      120      130      140      150      160      170

      100      110      120      130      140      150      160
ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATGTAGCCTGGTACCAACAGAAGCCAGGACAGTCTCCTAAACTGCTGATATACTATGCATCCAATCGCTACA
      180      190      200      210      220      230      240

      170      180      190      200      210      220      230
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTTTCACCATCAGCACTGTGCAGG
      250      260      270      280      290      300      310

      240      250      260      270      280      290      300      310
CTGAAGACCTGGCAGTTTATTTCTGTGTCAGCAGGATTATAGCTCTCCGTACACGTTCCGAGGGGGACCAAGC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TTGAAGACCTGGCAGTTTATTTCTGTGTCAGCAGCATTATAGCTCTCCGTGGACGTTCCGTGGAGGCACCAAGC
      320      330      340      350      360      370      380

      X
TGGAGATC
|||||
TGGAAATCAAA
390      X

```

5. US-07-977-702-2 (1-318)

MUSIGKCPF Mouse Ig active kappa-chain (V-J-C) mRNA from C.C5

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LOCUS      MUSIGKCPF      938 bp ss-mRNA      ROD      15-SEP-1989
DEFINITION Mouse Ig active kappa-chain (V-J-C) mRNA from C.C58 m75 myeloma.
ACCESSION  M12177
KEYWORDS   constant region; immunoglobulin light chain; immunoglobulin-kappa;
           joining region; processed gene; variable region.
SOURCE      Mouse C.C58 m75 myeloma cDNA to mRNA, clone p9.
ORGANISM    Mus musculus
           Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
           Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1 (bases 1 to 938)
AUTHORS     Goldrick,M.M., Boyd,R.T., Ponath,P.D., Lou,S.Y. and Gottlieb,P.D.
TITLE       Molecular genetic analysis of the VkSer group associated with two
           mouse light chain genetic markers
JOURNAL     J. Exp. Med. 162, 713-728 (1985)
STANDARD    full automatic
FEATURES     Location/Qualifiers
           sig_peptide      36..95
                       /codon_start=1
                       /note="Ig kappa chain (V-J-C) signal peptide"
           mat_peptide      96..737
                       /codon_start=1
                       /note="Ig kappa chain (V-J-C) mature peptide"
           misc_recomb      380..381
                       /note="V region end/J region start"
           misc_recomb      416..417
                       /note="J region end/C region start"
           CDS              36..739
                       /partial
                       /note="Ig kappa chain; (V-J-C)"
                       /codon_start=1
                       /translation="MKSQTQVFIFLLLCVSGAHGSIVHTQTPKFLPVSAGDRVMTCK
           ASQSVGNVVAWYQKPGQSPKLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVED

```

LOCUS	MMIGKL	938 bp	RNA	RDD	07-MAY-1992
DEFINITION	Mouse mRNA for Ig C.C58 M75 kappa light chain (VK Ser-group)				
ACCESSION	X02816 M12177				
KEYWORDS	constant region; Ig light chain; immunoglobulin; joining region; signal peptide; variable region.				
SOURCE	mouse				
ORGANISM	Mus musculus				
	Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.				
REFERENCE	1 (bases 1 to 938)				
AUTHORS	Goldrick,M.M., Boyd,R.T., Ponath,P.D., Lou,S.Y. and Gottlieb,P.D.				
TITLE	Molecular genetic analysis of the VkSer group associated with two mouse light chain genetic markers				
JOURNAL	J. Exp. Med. 162, 713-728 (1985)				
STANDARD	full automatic				
COMMENT	BALB/C mice germline V(K1) region see MMIG25, C(K) region see				

Data kindly reviewed (24-FEB-1986) by P.D. Gottlieb.

FEATURES Location/Qualifiers

misc_feature 165..197
/note="put. CDR1"

misc_feature 243..263
/note="put. CDR2"

misc_feature 360..380
/note="put. CDR3"

misc_feature 381..382
/note="CC is TG in germline J(K1) of BALB/ C"

misc_feature 416
/note="T is A in germline J(K1) of BALB/C"

misc_feature 710
/note="C is T in germline C(K) of BALB/C"

CDS 36..737
/note="(K)L-chain precursor"
/codon_start=1
/translation="MKSQTQVFIFLLLCVSGAHGSIVMTQTPKFLPVSAGDRVMTCK
ASQSVGNNAVWYQKPGQSPKLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVED
LAVYFCQGHYTSPTFGGGTKLEINRAAAPTVSIFPPSSEQLTSGGASVVCFLNNFY
PKDINVKWKIDGSRQNGVLNSWTDQDSKDYMSSTLTLTKEVERHNSYTCEATH
KTSTSPIVKSFNRECE"

CDS 36..95
/note="signal peptide; (aa -20 to -1)"
/codon_start=1
/translation="MKSQTQVFIFLLLCVSGAHC"

CDS 96..737
/note="mature; (K)L-chain (aa 1-214)"
/codon_start=1
/translation="SIVMTQTPKFLPVSAGDRVMTCKASQSVGNNAVWYQKPGQSP
KLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVEDLAVYFCQGHYTSPTFGGGT
KLEINRAAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVL
NSWTDQDSKDYMSSTLTLTKEVERHNSYTCEATHKTSTSPIVKSFNRECE"

CDS 96..380
/note="V region"
/codon_start=1
/translation="SIVMTQTPKFLPVSAGDRVMTCKASQSVGNNAVWYQKPGQSP
KLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVEDLAVYFCQGHYTSP"

CDS 381..416
/note="J region"
/codon_start=1
/translation="PTFGGGTKLEIN"

CDS 417..737
/note="C region"
/codon_start=1
/translation="RAAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKID
GSRQNGVLNSWTDQDSKDYMSSTLTLTKEVERHNSYTCEATHKTSTSPIVKSF
NRNECE"

BASE COUNT 248 a 260 c 206 g 224 t

ORIGIN

Initial Score = 290 Optimized Score = 293 Significance = 23.17

Residue Identity = 92% Matches = 293 Mismatches = 25

Gaps = 0 Conservative Substitutions = 0

X 10 20

AGTATTGTGATGACCCAGACTC

||||||||||||||||||||

AGACCCAGGTCTTCATATTTCTACTGCTCTGTGTCTGGTGCTCATGGGAGTATTGTGATGACCCAGACTC

50 60 70 80 90 X 100 110

30 40 50 60 70 80 90

CCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG

||||||||||| ||| ||||||||||||||||||| ||||||||||||||||||| ||||

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CCAAATTCCTGCTGATACAGGACAGGGTTACCATGACCTGCAAGGCCAGTCAGAGTGTGGGTAATA
120      130      140      150      160      170      180

      100      110      120      130      140      150      160
ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
ATGTAGCCTGGTACCAACAGAAGCCAGGACAGTCTCCTAAATTGCTGATATACTATGCATCCAATCGCTACA
190      200      210      220      230      240      250      260

      170      180      190      200      210      220      230
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTACCATCAGCACTGTGCAGG
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTTTACCATCAGCACTGTGCAGG
      270      280      290      300      310      320      330

240      250      260      270      280      290      300      310
CTGAAGACCTGGCAGTTTATTTCTGTGTCAGCAGGATTATAGCTCTCCGTACACGTTCCGAGGGGGGACCAAGC
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
TTGAAGACCTGGCAGTTTATTTCTGTGTCAGCAACATTATACCTCTCCTCCGACGTTCCGTGGAGGCACCAAGC
      340      350      360      370      380      390      400

      X
TGGAGATC
|||||
TGGAAATCAATCGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGA
      410 X      420      430      440      450      460

```

7. US-07-977-702-2 (1-318)

S60946 mAb BA.N4:4.57 V kappa region [mice, B cell hybrid

```

LOCUS      S60946      300 bp      mRNA      ROD      08-JAN-1992
DEFINITION mAb BA.N4:4.57 V kappa region [mice, B cell hybridoma, BALB/c,
            mRNA, 300 nt]
ACCESSION  S60946
KEYWORDS
SOURCE     mice BALB/c B cell hybridoma
ORGANISM   Unclassified.
            Unclassified.
REFERENCE  1 (bases 1 to 300)
AUTHORS    Carlsson,L., Andersson,A. and Holmberg,D.
TITLE      Germ-line origin of functional idiotypic interactions:
            identification of two idiotypically connected, natural antibodies
            that are encoded by germ-line gene elements.
JOURNAL    Eur. J. Immunol. 21, 2285-2288 (1991)
STANDARD   full automatic
COMMENT    This entry [NCBI gibbsq 60946] was created by the journal scanning
            component of NCBI/GenBank at the National Library of Medicine.
            This sequence comes from Fig.2.
FEATURES   Location/Qualifiers
            misc_feature 1..300
                        /note="This feature applies to a gene which lacks a coding
                        region feature. Description: mAb BA.N4:4.57 V kappa
                        region"
BASE COUNT 74 a      69 c      77 g      77 t      3 others
ORIGIN

```

Initial Score = 287 Optimized Score = 289 Significance = 22.91
Residue Identity = 96% Matches = 289 Mismatches = 11
Gaps = 0 Conservative Substitutions = 0

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X      10      20      30      40      50      60      70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
AGTATTGTGATGACCCAGACTCCNNAATTCCTGCTTGTATCAGCAGGAGAGAGGGTTACCATAACCTGCAAG
X      10      20      30      40      50      60      70

```

```

      80      90      100      110      120      130      140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
|||||
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
      80      90      100      110      120      130      140

      150      160      170      180      190      200      210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
TACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
      150      160      170      180      190      200      210

      220      230      240      250      260      270      280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTAC
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGNAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTGG
      220      230      240      250      260      270      280

290      X      310
ACGTTTCGGAGGGGGACCAAGCTGGAGATC
|||||
ACGTTTCGGTGGGA
290      300

```

8. US-07-977-702-2 (1-318)

MMVL105 Mouse mRNA for kappa-immunoglobulin light chain V-

```

LOCUS      MMVL105      321 bp      RNA      ROD      04-AUG-1992
DEFINITION Mouse mRNA for kappa-immunoglobulin light chain V-J region (cell
line 105-2H)
ACCESSION  X51852
KEYWORDS   Ig kappa light chain; Ig light chain; immunoglobulin;
joining region; variable region.
SOURCE      mouse
ORGANISM    Mus musculus
Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE  1 (bases 1 to 321)
AUTHORS     Reininger,L.
TITLE       Direct Submission
JOURNAL     Submitted (16-FEB-1990) Reininger L., Dept of Pathology , Centre
Medical Universitaire, 1 rue michel servet, CH-1211 Geneve 4,
Switzerland.
STANDARD    full automatic
REFERENCE  2 (bases 1 to 321)
AUTHORS     Reininger,L., Shibata,T., Ozaki,S., Shirai,T., Jatou,J.C. and
Izui,S.
TITLE       Variable region sequences of pathogenic anti-mouse red blood cell
autoantibodies from autoimmune NZB mice.
JOURNAL     Eur. J. Immunol. 20, 771-777 (1990)
STANDARD    full automatic
COMMENT     *source: strain=New Zealand black; *source: cell_type=hybridoma B;

*source: cell_line=105-2H.
FEATURES
  CDS
    <1..321
    /note="kappa-Ig light chain (107 AA)"
BASE COUNT  81 a      72 c      82 g      78 t      8 others
ORIGIN

```

Initial Score = 287 Optimized Score = 290 Significance = 22.91
Residue Identity = 91% Matches = 291 Mismatches = 26
Gaps = 1 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAA
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GAG-ATTGTGTTGACCCAGACTCCNNAATTCCTGCTTGATCAGTAGGAGACAGGGTTACCATAACCTGCNA
X      10      20      30      40      50      60      70

      80      90      100      110      120      130      140
GGCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGAT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GGCCAGTCAGAGTGTGAAGAATGATGTTGGNTGGTACCAACAGNAGCCAGGGCAGTCTCCTAAATTGCTGAT
      80      90      100      110      120      130      140

      150      160      170      180      190      200      210
ATATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATACTATGCATCCAATCGCTACACTGGAATCCCTGATCGCTTCACTGGCAGTGGACATGGGACGGATTTCAC
      150      160      170      180      190      200      210

      220      230      240      250      260      270      280
TTTCACCATCAGCACTGTGCGAGGCTGAAGACCTGGCAGTTTATTTCTGTCTCAGCAGGATTATAGCTCTCCGTA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TTTCACCATCAGCACTGTGCGAGGCTGAAGACCTGGNNGTTTATTTCTGTCTCAGCAGGATNATACCTCTCCGTA
      220      230      240      250      260      270      280

290      300      310      X
CACGTTCGGAGGGGGGACCAAGCTGGAGATC
||||| || ||||| ||||| ||
GACGTTGGTGGAGGGACCAAGCTGGAATAAAA
290      300      310      320

```

9. US-07-977-702-2 (1-318)

MUSIGKVM Mouse Ig germline kappa-chain V-region gene V-Ser.

```

LOCUS      MUSIGKVM      1816 bp ds-DNA      ROD      30-JUN-1987
DEFINITION Mouse Ig germline kappa-chain V-region gene V-Ser.
ACCESSION  M14360
KEYWORDS   constant region; germline; immunoglobulin-kappa; variable region.
SOURCE      Mouse (Balb/c) liver DNA, clone EM3.BALB-1.
ORGANISM    Mus musculus
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1 (bases 1 to 1816)
AUTHORS     Boyd,R.T., Goldrick,M.M. and Gottlieb,P.D.
TITLE        Structural differences in a single gene encoding the V-k-Ser group
             of light chains explain the existence of two mouse light-chain
             genetic markers
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138 (1986)
STANDARD     full automatic
FEATURES     Location/Qualifiers
             exon
             <916..964
             /number=1
             /note="Ig kappa-chain precursor V-Ser"
             sig_peptide
             join(916..964,1179..1189)
             /codon_start=1
             /note="Ig kappa-chain signal peptide"
             sig_peptide
             916..964
             /codon_start=1
             /note="Ig kappa-chain signal peptide"
             intron
             965..1178
             /note="IgK intron A"
             exon
             1179..>1474
             /number=2
             /note="Ig kappa-chain precursor V-Ser"
             sig_peptide
             1179..1189
             /codon_start=1

```

```

mat_peptide 1190..1474
              /note="Ig kappa-chain signal peptide"
              /partial
              /codon_start=1
              /note="Ig kappa-chain"
idNA         1475..>1816
              /note="V-J intervening DNA (5' end +/- 1 bp)"
CDS          join(916..964,1179..1473)
              /partial
              /partial
              /note="Ig kappa-chain precursor V-Ser"
              /codon_start=1
              /translation="MKSQTQVFVFLLCVSGAHGSIVMTQTPKFLLVSAGERVTITCK
ASQSVSNDAWYQQKPGQSPKLLIYYASNRYTGVDPDRFTGSGYGTDFTFITSTVQAE
LAVYFCQQDYSSP"
BASE COUNT   482 a   385 c   354 g   595 t
ORIGIN       1297 bp upstream of KpnI site; chromosome 6.

```

```

Initial Score = 280 Optimized Score = 294 Significance = 22.29
Residue Identity = 92% Matches = 301 Mismatches = 17
Gaps = 9 Conservative Substitutions = 0

```

```

                                X      10      20
                                AGTATTGTGATGACCCAGACTC
                                |||
GTGTAAATGTGTATCCTCATTATTTATCTCTGATTGCAGGTGCTCATGGGAGTATTGTGATGACCCAGACTC
1140      1150      1160      1170      1180      1190      1200      1210

      30      40      50      60      70      80      90
CCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
|||
CCAAATTCCTGCTTGTATCAGCAGGAGAGAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATG
1220      1230      1240      1250      1260      1270      1280

      100      110      120      130      140      150      160
ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
|||
ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATACTATGCATCCAATCGCTACA
1290      1300      1310      1320      1330      1340      1350

      170      180      190      200      210      220      230
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
|||
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
1360      1370      1380      1390      1400      1410      1420

      240      250      260      270      280      290      300
CTGAAGACCTGGCAGTTTATTTCTGTGTCAGCAGGATTATAGCTCTCCGTACAC-GTTC-GGAG-GGGGGAC-C
|||
CTGAAGACCTGGCAGTTTATTTCTGTGTCAGCAGGATTATAGCTCTCCTCCACAGTGCTTCAGCCTCCTACAC
1430      1440      1450      1460      1470      1480      1490

      310      X
AA----GCTGGAGA-TC
||
AAACCTCCTTGAGAGTCTCACAGCTGTGGCCTTGACAGTTCCTCCCTCTGCCTGGAGCAGCGATTCA
1500      1510      1520      1530      1540      1550      1560

```

10. US-07-977-702-2 (1-318)

S60873 Ab2 kappa chain V region | mAb F {V/J junction} [m

```

LOCUS       S60873      300 bp      mRNA           ROD      08-JAN-1992
DEFINITION  Ab2 kappa chain V region | mAb F {V/J junction} [mice, MLR-lpr/lpr,
              mRNA Partial, 300 nt]
ACCESSION   S60873

```

KEYWORDS .
SOURCE mice MLR-lpr/lpr
ORGANISM Unclassified.
Unclassified.
REFERENCE 1 (bases 1 to 300)
AUTHORS Koizumi,T., Puccetti,A., Migliorini,P., Barrett,K.J. and
Schwartz,R.S.
TITLE Molecular heterogeneity of auto-anti-idiotypic antibodies in
MLR-lpr/lpr mice.
JOURNAL Eur. J. Immunol. 21, 2185-2193 (1991)
STANDARD full automatic
COMMENT This entry [NCBI gibbsq 60873] was created by the journal scanning
component of NCBI/GenBank at the National Library of Medicine.
This sequence comes from Fig.6.
FEATURES Location/Qualifiers
misc_feature 1..300
/note="This feature applies to a gene which lacks a coding
region feature. Description: Ab2 kappa chain V region |
mAb F"
BASE COUNT 74 a 77 c 71 g 76 t 2 others
ORIGIN

Initial Score = 278 Optimized Score = 279 Significance = 22.11
Residue Identity = 93% Matches = 279 Mismatches = 21
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
|||||
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCATGACCTGCAAG
X 10 20 30 40 50 60 70

80 90 100 110 120 130 140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
|||||
GCCAGTCAGAGTGTGGTAATAATGTAGCCTGGTACCAACAGAAGCCAGGACAGTCTCCTAANCTGCTGATA
80 90 100 110 120 130 140

150 160 170 180 190 200 210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCCT
||
TACTATGCATCCAATCGCTACACTGGNGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCCT
150 160 170 180 190 200 210

220 230 240 250 260 270 280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCTCAGCAGGATTATAGCTCTCCGTAC
|||||
TTCACCATCAGCAGTGTGCAGGTTGAAGACCTGGCAGTTTATTTCTGTCTCAGCAGATTATAGCTCTCCATT
220 230 240 250 260 270 280

290 X 310
ACGTTCTGGAGGGGGACCAAGCTGGAGATC
|||||
ACGTTCTGGCAGC
290 300

11. US-07-977-702-2 (1-318)

MMNPCRLB6 M.musculus NPCRLB6 mRNA for immunoglobulin light c

ID MMNPCRLB6 standard; RNA; ROD; 321 BP.
XX
AC X70097; X51612;
XX
DT 19-MAR-1993 (Rel. 35, Created)
DT 19-MAR-1993 (Rel. 35, Last updated, Version 1)

XX
 DE M.musculus NPCRLB6 mRNA for immunoglobulin light chain, variable
 DE region
 XX
 KW immunoglobulin light chain variable region.
 XX
 OS Mus musculus (mouse)
 DC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 DC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 XX
 RN [1]
 RP 1-321
 RA Izui S.;
 RT ;
 RL Submitted (05-FEB-1993) on tape to the EMBL Data Library by:
 RL S. Izui, Dept. of Pathology, Centre Medical Universitaire, 1. Rue
 RL Michel Servet, CH-1211, geneva 4, SWITZERLAND
 XX
 CC *source: strain=C57BL/6;
 CC *source: tissue=lymphoid;
 CC *source: cell_type=hybridoma;
 CC *source: cell_line=CB6;
 CC *source: is_germline=N;
 XX
 FH Key Location/Qualifiers
 FH
 FT CDS <1..>321
 FT /codon_start=1
 FT /product="immunoglobulin light chain, variable region"
 XX
 SQ Sequence 321 BP; 88 A; 80 C; 78 G; 75 T; 0 other;

Initial Score = 273 Optimized Score = 275 Significance = 21.67
 Residue Identity = 86% Matches = 275 Mismatches = 43
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
|||||
GACATTGTGATGACCCAGTCTCACAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAG
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
|||||
GCCAGTCAGGATGTGAGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGACAATCTCCTAAACTACTGATT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTCTACT
|||
TACTCGGCATCCTACCGGTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACGGATTCTACT
     150     160     170     180     190     200     210

    220     230     240     250     260     270     280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTCTGTCTCAGCAGGATTATAGCTCTCCGTAC
|||||
TTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCTCAGCAACATTATAGTACTCCGTAC
    220     230     240     250     260     270     280

    290     300     310     X
ACGTTCTGGAGGGGGGACCAAGCTGGAGATC
|||||
ACGTTCTGGAGGGGGGACCAAGCTGGAATAAAA
    290     300     310     320
  
```

12. US-07-977-702-2 (1-318)

MUSIGKCNK Mouse Ig rearranged kappa-chain mRNA, clone AN12K.

LOCUS MUSIGKCNK 456 bp ss-mRNA ROD 15-MAR-1990
 DEFINITION Mouse Ig rearranged kappa-chain mRNA, clone AN12K.
 ACCESSION M19914 J03832
 KEYWORDS constant region; immunoglobulin light chain; immunoglobulin-kappa;
 processed gene.
 SOURCE Mouse (BALB/c) mature B cell, cDNA to mRNA, clone AN12K.
 ORGANISM Mus musculus
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
 Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE 1 (bases 1 to 56)
 AUTHORS Rule,G.S.
 JOURNAL Unpublished (1988) Stanford U., Chem. Dept., Stanford CA 94305.
 STANDARD full automatic
 REFERENCE 2 (bases 1 to 456)
 AUTHORS Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.
 TITLE Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-bodies
 for NMR studies
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)
 STANDARD full automatic
 COMMENT Draft entry and computer-readable sequence [2] kindly submitted by
 G.Rule, 20-JUL-1988.

FEATURES Location/Qualifiers
 sig_peptide 19..90
 /codon_start=1
 /note="Ig kappa-chain signal peptide"
 mat_peptide 91..456
 /partial
 /codon_start=1
 /note="Ig kappa-chain"
 CDS 19..455
 /partial
 /partial
 /note="Ig kappa-chain precursor"
 /codon_start=1
 /translation="MGIKMESQIQVFVFLWLSGVGDIVMTQSHKFMSTSVGDRVS
 ITCKASQDVSTAVAWYQKPGQSPKLLIYSASYRYTGVPDRFTGSGSGTDFTFTISSV
 QAEDLAVYYCHQHYSSPYTFGGGTKLEIKRADAAPTVSIFPPSX"

BASE COUNT 118 a 114 c 108 g 116 t
 ORIGIN

Initial Score = 272 Optimized Score = 275 Significance = 21.58
 Residue Identity = 86% Matches = 276 Mismatches = 42
 Gaps = 1 Conservative Substitutions = 0

```

                                X      10      20
                                AG-TATTGTGATGACCCAGACT
                                || ||||| ||||| ||
CAGATTCAGGTCTTTGTATTCTGTTTCTCTGGTTGTCTGGTGTGACGGAGACATTGTGATGACCCAGTCT
40      50      60      70      80      90      100     110

      30      40      50      60      70      80      90
CCCAAATTCCTGCTTGTGTTTCAGCAGGAGACAGGGTTACCATAACTGCAAGGCCAGTCAGAGTGTGACTAAT
| ||||| || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CACAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGAGTACT
120     130     140     150     160     170     180

      100     110     120     130     140     150     160
GATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAACTGCTGATATATTGCATCCAATCGCTAC
| ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GCTGTAGCCTGGTATCAACAAAAACCAGGACAATCTCCTAACTACTGATTTACTCGGCATCTACCGGTAC
190     200     210     220     230     240     250

```

```

170      180      190      200      210      220      230
ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACCTTCACCATCAGCACTGTGCAG
|||||
ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACGGATTTCACCTTCACCATCAGCACTGTGCAG
260      270      280      290      300      310      320

240      250      260      270      280      290      300
GCTGAAGACCTGGCAGTTTATTTCTGTCTCAGCAGGATTATAGCTCTCCGTACACGTTCCGAGGGGGGACCAAG
|||||
GCTGAAGACCTGGCAGTTTATTACTGTCTATCAACATTATAGTTCTCCGTACACGTTCCGAGGGGGGACCAAG
330      340      350      360      370      380      390

310      X
CTGGAGATC
|||||
CTGGAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGT
400      410      420      430      440      450

```

13. US-07-977-702-2 (1-318)

MMNPCRLB1 M.musculus NPCRLB1 mRNA for immunoglobulin light c

```

ID  MMNPCRLB1 standard; RNA; ROD; 321 BP.
XX
AC  X70095; X51612;
XX
DT  19-MAR-1993 (Rel. 35, Created)
DT  19-MAR-1993 (Rel. 35, Last updated, Version 1)
XX
DE  M.musculus NPCRLB1 mRNA for immunoglobulin light chain, variable
DE  region
XX
KW  immunoglobulin light chain variable region.
XX
OS  Mus musculus (mouse)
OC  Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC  Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
XX
RN  [1]
RP  1-321
RA  Izui S.;
RT  ;
RL  Submitted (05-FEB-1993) on tape to the EMBL Data Library by:
RL  S. Izui, Dept. of Pathology, Centre Medical Universitaire, 1, Rue
RL  Michel Servet, CH-1211, geneva 4, SWITZERLAND
XX
CC  *source: strain=C57BL/6;
CC  *source: tissue=lymphoid;
CC  *source: cell_type=hybridoma;
CC  *source: cell_line=CB1;
CC  *source: is_germline=N;
XX
FH  Key          Location/Qualifiers
FH
FT  CDS          <1..>321
FT              /codon_start=1
FT              /product="immunoglobulin light chain, variable region"
XX
SQ  Sequence 321 BP; 87 A; 81 C; 77 G; 76 T; 0 other;

```

```

Initial Score   =   271  Optimized Score   =   273  Significance = 21.50
Residue Identity =   85%  Matches           =   273  Mismatches   =   45
Gaps            =       0  Conservative Substitutions   =       0

```

```

X      10      20      30      40      50      60      70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG

```

```

|||||
GACATTGTGATGACCCAGTCTCACAATTTCATGTCCACATCAGTTGGAGACAGGGTCAGCATCACCTGCAAG
X      10      20      30      40      50      60      70

      80      90      100      110      120      130      140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
||||| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GCCAGTCAGGATGTGAGTACTGCTGTAGCCCTGGTATCAACAGAAACCAGGACAATCTCCTAAACTACTGATT
      80      90      100      110      120      130      140

      150      160      170      180      190      200      210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
T || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TACTCGGCATCCTACCGGTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACGGATTTCAC
      150      160      170      180      190      200      210

      220      230      240      250      260      270      280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTGAGCAGGATTATAGCTCTCGGTAC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TTCACCATCAGCAGTGTGCAGCCTGAAGACCTGGCAGTTTATTACTGTGAGCAACATTATAGTACTCGGTAC
      220      230      240      250      260      270      280

290      300      310      X
ACGTTTCGGAGGGGGGACCAAGCTGGAGATC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ACGTTTCGGAGGGGGGACCAAGCTGGAATAAAA
290      300      310      320

```

14. US-07-977-702-2 (1-318)

MUSIGKVN Mouse Ig germline kappa-chain V-region gene V-Ser.

LOCUS MUSIGKVN 2002 bp ds-DNA ROD 30-JUN-1987

DEFINITION Mouse Ig germline kappa-chain V-region gene V-Ser.

ACCESSION M14361

KEYWORDS constant region; germline; immunoglobulin-kappa; variable region.

SOURCE Mouse (C.C58) liver DNA, clones EMC58-[5,7,10].

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 2002)

AUTHORS Boyd,R.T., Goldrick,M.M. and Gottlieb,P.D.

TITLE Structural differences in a single gene encoding the V-k-Ser group
of light chains explain the existence of two mouse light-chain
genetic markers

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138 (1986)

STANDARD full automatic

FEATURES Location/Qualifiers

exon	<1071..1119
	/number=1
	/note="Ig kappa-chain precursor V-Ser"
sig_peptide	join(1071..1119,1335..1346)
	/codon_start=1
	/note="Ig kappa-chain signal peptide"
sig_peptide	1071..1119
	/codon_start=1
	/note="Ig kappa-chain signal peptide"
intron	1120..1334
	/note="IgK intron A"
exon	1335..>1630
	/number=2
	/note="Ig kappa-chain precursor V-Ser"
sig_peptide	1335..1346
	/codon_start=1
	/note="Ig kappa-chain signal peptide"
mat_peptide	1347..1630

```

partial
/codon_start=1
/note="Ig kappa-chain"
iDNA 1631..>2002
/note="V-J intervening DNA (5' end +/- 1 bp)"
CDS join(1071..1119,1335..1629)
/partial
/partial
/note="Ig kappa-chain precursor V-Ser"
/codon_start=1
/translation="MKSQTQVFIFLLLCVSGAHGSIVMTQTPKFLPVSAGDRVMTCK
ASQSVGNVAVYGGKPGQSPKLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVED
LAVYFCQQHYSSP"

```

BASE COUNT 533 a 421 c 376 g 672 t
 ORIGIN 1 bp upstream of EcoRI site; chromosome 6.

Initial Score = 270 Optimized Score = 284 Significance = 21.41
 Residue Identity = 88% Matches = 291 Mismatches = 27
 Gaps = 9 Conservative Substitutions = 0

```

                                X      10      20
                                AGTATTGTGATGACCCAGACTC
                                |||||
GTGTAAATGTGTATCCTCATTATTTATCTCTGATTGCAGGTGCTCATGGGAGTATTGTGATGACCCAGACTC
1300      1310      1320      1330      1340      1350      1360

      30      40      50      60      70      80      90
CCAAATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
||||| ||| |||||
CCAAATTCCTGCTGATCAGCAGGAGACAGGGTTACCATGACCTGCAAGGCCAGTCAGAGTGTGGTAATA
1370      1380      1390      1400      1410      1420      1430

      100      110      120      130      140      150      160
ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
||||| |||||
ATGTAGCCTGGTACCAACAGAAGCCAGGACAGTCTCCTAAACTGCTGATATACTATGCATCCAATCGCTACA
1440      1450      1460      1470      1480      1490      1500      1510

      170      180      190      200      210      220      230
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
||||| |||||
CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTTTCACCATCAGCACTGTGCAGG
1520      1530      1540      1550      1560      1570      1580

      240      250      260      270      280      290      300
CTGAAGACCTGGCAGTTTATTTCTGTGTCAGCAGGATTATAGCTCTCCGTACAC-GTTC-GGAG-GGGGGAC-C
||||| ||||| ||| || | ||
TTGAAGACCTGGCAGTTTATTTCTGTGTCAGCAGCATTATAGCTCTCCTCCCAGTGTTCAGCCTCCTACAC
1590      1600      1610      1620      1630      1640      1650

      310      X
AA----GCTGGAGA-TC
|| || ||| ||
AAACCTCCTTGAGAGTCTCACAGCTGCCTGTCTACATACAGCTGTGGCCTTGACACTTCCCCCTC
1660      1670 X 1680      1690      1700      1710      1720

```

15. US-07-977-702-2 (1-318)

MUSIGKCKP Mouse Ig kappa-chain mRNA V-region (VJ), from hybr

LOCUS MUSIGKCKP 341 bp ss-mRNA ROD 15-MAR-1989
 DEFINITION Mouse Ig kappa-chain mRNA V-region (VJ), from hybridoma
 A003-40/5G7k.
 ACCESSION M17161 J02815
 KEYWORDS immunoglobulin light chain; immunoglobulin-kappa; joining region;
 variable region.

